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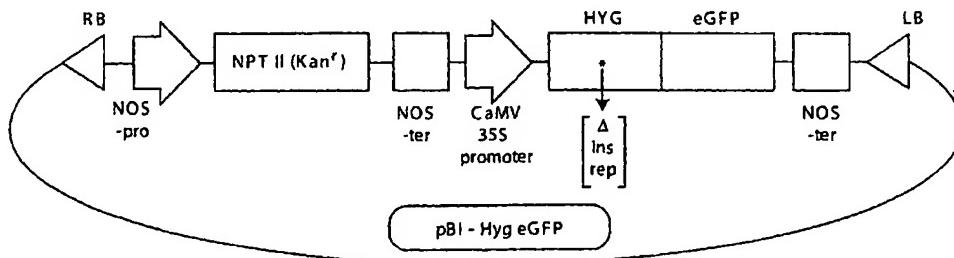
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(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES



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(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclelease-resistant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.



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**TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS
USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES**

Field Of The Invention

5 The technical field of the invention is oligonucleotide-directed repair or alteration of plant genetic information using novel chemically modified oligonucleotides.

Background Of The Invention

A number of methods have been developed specifically to alter the genomic information of plants. These methods generally include the use of vectors such as, for example, T-DNA, carrying nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in 10 a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. See, for example, United States Patent 4,459,355 which describes a method for transforming plants with a DNA vector and United States Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene-containing vectors adds one or more exogenous copies 15 of a gene in a usually random fashion at one or more integration sites of the plant's genome at some variable frequency. The introduced gene may be foreign or may be derived from the host plant. Any gene which was originally present in the genome, which may be, for example, a normal allelic variant, mutated, defective, and/or functional copy of the introduced gene, is retained in the genome of the host plant.

20 These methods of gene alteration are problematic in that complications which can compromise the vigor, productivity, yield, etc. of the plant may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. The random nature of this insertion and/or the use of exogenous promoters can also cause the timing, location or strength of expression of the introduced transgene to be inappropriate or unpredictable. Another problem 25 with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, T-DNA ends or other vector remnants, exogenous control sequences required to allow production of the transgene protein, which control sequences may be

exogenous or native to the host plant and/or the transgene, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. In addition, concerns have been raised with consumption, especially by humans, of plants containing such exogenous genetic material.

5 More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant, animal or fungal genomes. See, for example, WO 99/07865 and U.S. Patent
10 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene
15 alteration, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result reduces the utility of such a molecule in methods designed for targeted gene alteration.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide.
20 Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of
25 these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.
30

Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Similar efforts to target genes by homologous recombination in plants using large fragments of DNA had some success. See Kempin et al., Nature 389:802-803 (1997). However, the efficiency and reproducibility of the published homologous recombination approach in plants has severely limited the widespread use of this method.

Earlier experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide rather than larger fragments of DNA, wherein the oligonucleotide had no functional domains other than a region of complementary sequence to the target. See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

Oligonucleotides designed for use in the targeted alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to genomic sequences that span the junction between intron sequence and exon sequence.

Artificial chromosomes can be useful for the screening purposes identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large segments of genomic DNA to be cloned and modified (Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat.

Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)). Other vectors also have been developed for the cloning of large segments of genomic DNA, including cosmids, and bacteriophage P1 (Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)). YACs have certain advantages over these alternative large capacity cloning vectors (Burke et al., Science, 236:806-812 (1987)). The maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert size for a YAC.

An alternative to YACs are cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) (Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)). BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. The PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis (Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979)). In addition, BACs have been developed for transformation of plants with high-molecular weight DNA using the T-DNA system (Hamilton, *Gene* 24:107-116 (1997); Frary & Hamilton, *Transgenic Res.* 10: 121-132 (2001)).

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants are identified and the efficiency of alteration is analyzed both *in vitro* using a cell-free extract assay and *in vivo* using a yeast system and a plant system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site specific alteration of DNA is not only useful for studying function of proteins *in vivo*, but it is also useful for creating plants with desired phenotypes, including, for example, environmental stress tolerance, improved nutritional value, herbicide resistance, disease resistance, modified oil production, modified starch production, and altered floral morphology including selective sterility. As described herein,

oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA in cells. The target genomic DNA can be nuclear chromosomal DNA as well as plastid or mitochondrial chromosomal DNA. The target DNA can also be a transgene present in the plant cell, including; for example, a previously introduced T-DNA. For screening purposes, the target plant DNA can 5 also be extrachromosomal DNA present in plant or non-plant cells in various forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing plant DNA can be obtained from a variety of sources, 10 including, e.g., the Arabidopsis Biological Resource Center (ABRC) at the Ohio State University, and the Rice Genome Research Program at the MAFF DNA bank in Ibaraki, Japan. The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex. In a more preferred embodiment, the target DNA to be altered is the non-transcribed strand of a transcribed gene of a genomic DNA duplex.

15 The low efficiency of targeted gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., *J. Am. Chem. Soc.*, 120:13252-3), we have found that it is not possible to predict 20 which of any particular known modification would be most useful for any given alteration event, including for the construction of gene alteration oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that 25 single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See, for example, copending applications United States application no. 60/208,538, United States application no. 60/244,989, United States application no. 09/818,875, international application no. PCT/US01/09761 and Gamper et al., 30 Nucleic Acids Research 28: 4332-4339 (2000), the disclosures of which are incorporated herein in their entirety by reference. We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-

LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748; Wengel, WO 00/66604; and Jakobsen & Koskin, WO 01/25478 also allow specific targeted alteration of genetic information.

The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different plants or strains, or testing cells derived from different plants or strains, or plant cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an *in vitro* gene repair assay. Similar results are also observed *in vivo* using yeast, mammalian and plant cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

25 **Detailed Description Of The Invention**

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of plant genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration,

including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity. For example, gene alterations that knockout a particular protein activity can be obtained using oligonucleotides designed to convert a codon in the coding region of the protein to a stop codon, thus prematurely terminating translation of the protein. Oligonucleotides that introduce stop codons in the open-reading-frame of the protein are one embodiment of the invention. Generally, oligonucleotides that introduce stop codons early in the open-reading-frame of the protein are preferred. If the open-reading-frame contains more than one methionine, oligonucleotides that introduce stop codons after the second methionine are preferred. Additionally, if the gene exhibits alternative splice sites, oligonucleotides that introduce stop codons in exons after the alternative splice site are preferred. The following table provides examples of codons that can be converted to stop codons by altering a single oligonucleotide. A skilled artisan could readily identify other codons that can be converted to stop codons by altering one, two or three of the base pairs in a given codon. Similarly, a skilled artisan could readily identify codons that can be converted to stop codons by a frameshift mutations that inserts or deletes one or two base pairs in the open-reading-frame. It is also understood that more than one stop codon can be generated in a single open-reading-frame and that these stop codons can be adjacent in the sequence or separated by intervening codons. Where more than one stop codon is introduced into a single open-reading-frame, such alterations can be generated by a single or multiple oligonucleotides and can be generated simultaneously or by sequential mutagenesis of the target nucleic acid.

	Original codons*	Corresponding stop codon
20	<u>G</u> GA (glycine), <u>A</u> GA (arginine), <u>C</u> GA (arginine), <u>T</u> <u>T</u> A (leucine), <u>T</u> <u>C</u> A (serine), <u>T</u> <u>G</u> T (cysteine), <u>T</u> <u>G</u> <u>G</u> (tryptophan), <u>T</u> <u>G</u> <u>C</u> (cysteine)	TGA
15	<u>A</u> AG (lysine), <u>G</u> AG (glutamate), <u>C</u> AG (glutamine), <u>T</u> <u>T</u> G (leucine), <u>T</u> <u>C</u> G (serine), <u>T</u> <u>G</u> <u>G</u> (tryptophan), <u>T</u> <u>A</u> <u>T</u> (cysteine), <u>T</u> <u>A</u> <u>C</u> (tyrosine)	TAG
25	<u>A</u> AA (lysine), <u>G</u> AA (glutamate), <u>C</u> AA (glutamine), <u>T</u> <u>T</u> A (leucine), <u>T</u> <u>C</u> A (serine), <u>T</u> <u>A</u> <u>T</u> (cysteine), <u>T</u> <u>A</u> <u>C</u> (tyrosine)	TAA

*The amino acid encoded by the original codon is shown in parentheses and the base targeted for alteration to convert the codon to the corresponding stop codon is underlined and in bold

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligo-
5 nucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain
10 surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region, are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Preferred oligonucleotides of the invention have at least two modified bases on at least one of the termini, preferably the 3' terminus of the oligonucleotide. Oligonucleotides
15 of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cells of different types including, for example, plant cells, fungal cells including *S. cerevisiae*, *Ustilago maydis*, *Candida albicans*, and mammalian cells. Particularly preferred are cells and cell extracts derived from plants including, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and
20 *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as
25 walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogaea*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyrus*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichoreum*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleraceae*), tobacco (*Nicotiana*, e.g.
30 *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds,

such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*),
5. chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceæ*), potato (*Solanum*, e.g. *tuberosum*) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. *x hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's
10 tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.). Such plant cells can then be used to regenerate whole plants according to methods described herein or any method known in the art. The DNA domain of the oligonucleotides is preferably
15 fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration event(s). On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

According to certain embodiments, one or both of the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone (including LNA derivatives and analogs) modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. The oligonucleotides of the invention are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA (including LNA derivatives or analogs), phosphorothioate linkages, or 2'-O-methyl analog incorporation into an oligonucleotide can not yet be predicted because the proteins
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involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, oligonucleotides of defined sequence are provided for alteration of genes in particular plants. Provided the teachings of the instant application, one of skill in the art could readily design oligonucleotides to introduce analogous alterations in homologous genes from any plant. Furthermore, in the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. In some embodiments, longer nucleic acids of up to 240 bases which comprise the sequences disclosed herein may be used. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for alteration of particular plant genes contain phosphorothioate linkages, 2'-O-methyl analog or LNA (including LNA derivatives and analogs) or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs (including LNA derivatives and analogs), phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having

phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4 analogs are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substrate molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired the desire change. The oligonucleotides of the invention in different embodiments can alter DNA two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery

which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either strand of DNA and can include any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene alteration activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide-dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the

same sequence alteration. Similarly, molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, preferably, using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241) (<http://www.idtdna.com>); this program is available for use on the world wide web at

<http://www.idtdna.com/program/oligoanalyzer/>

oligoanalyzer.asp.

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St, Madison, WI 53715, Phone: (608) 258-7420 (<http://www.dnastar.com/products/PrimerSelect.html>).

If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed

strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e. the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

The oligonucleotides of the invention can include more than a single base change. In an 5 oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain, within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target 10 bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the 15 oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine 20 (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. For plant cells, biolistic or particle bombardment methods are typically used. According to certain preferred embodiments of the present invention, isolated plant cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Alternatively, plant target DNA may be modified *in vitro* or in another cell type, including for example, yeast or bacterial cells and then introduced 25 into a plant cell as, for example, a T-DNA. Plant cells thus modified may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place *in vivo* following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

The single-stranded, modified oligonucleotides of the present invention have numerous 30 applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention

offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the genetic complement of the organism. Such agents may, for example, be used to develop plants with improved traits by rationally changing the sequence of selected genes in isolated cells and using these modified cells to regenerate whole plants having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated herein by reference. Such plants produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of plants having particular modified or inactivated genes. Altered plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used to introduce molecular markers, including, for example, SNPs, RFLPs, AFLPs and CAPs.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures depending on the target. For example, purified oligonucleotide can be used directly in a standard reaction mixture to introduce alterations into targeted DNA *in vitro* or where cells are the target as a composition adapted for bathing cells in culture or for microinjection into cells in culture. The purified oligonucleotide compositions may also be provided on coated microbeads for biolistic delivery into plant cells. Where necessary, the composition may also include a solubilizing agent. Generally, the ingredients will be supplied either separately or mixed together in single-use form, for example, as a dry, lyophilized powder or water-free concentrate. In general, dosage required for efficient targeted gene alteration will range from about 0.001 to 50,000 µg/kg target tissue, preferably between 1 to 250 µg/kg, and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve

efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein. For biolistic delivery, microbeads are generally coated with resuspended oligonucleotides, which range of oligonucleotide to microbead concentration can be similarly adjusted to improve efficiency as determined using one of the assay methods described herein, starting with about 5 0.05 to 1 microgram of oligonucleotide to 25 microgram of 1.0 micrometer gold beads or similar microcarrier.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an additional reagent or article of manufacture. The additional reagent or article of manufacture may comprise a delivery mechanism, cell extract, a cell, or a plasmid, such as 10 one of those disclosed in the Figures herein, for use in an assay of the invention. Alternatively, the invention includes a kit comprising an isogenic set of cells in which each cell in the kit comprises a different altered amino acid for a target protein encoded by a targeted altered gene within the cell produced according to the methods of the invention.

Brief Description Of The Drawings

15 Figure 1. *Flow diagram for the generation of modified single-stranded oligonucleotides.* The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene. The numbers 3, 6, 8, 10, 12 and 20 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 25 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

30 Figure 2. *Genetic readout system for correction of a point mutation in plasmid pK^sm4021.* A mutant kanamycin gene harbored in plasmid pK^sm4021 is the target for correction by oligonucleotides.

The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid pT^sΔ208 contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. *DNA sequences of representative kan' colonies.* Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(')FIAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a

base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function.

Figure 8. Oligonucleotides for correction of hygromycin resistance gene. The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

Figure 9. pAURNeo(-)FIAsh plasmid. This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

Figure 10. pYESHyg(x)eGFP plasmid. This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

Figure 11. pBI-HygeGFP plasmid. This plasmid is a construct based on the plasmids pBI101, pBI 101.2, pBI101.3 or pBI 121 available from Clontech in which HygeGFP replaces the beta-glucuronidase gene of the Clontech plasmids. The different Clontech plasmids vary by a reading frame shift relative to the polylinker, or the presence of the Cauliflower mosaic virus promoter.

The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

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EXAMPLE 1 Assay Method For Base Alteration And Preferred Oligonucleotide Selection

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK^sm4021 (Figure 2) or the tetracycline gene of pT^sΔ208 (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(-)FIAsh (Figure 9), bearing the kan^s gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase

(kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FlAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FlAsH fusion product (after alteration) or the truncated Neo-/FlAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy.

Additional constructs can be made to test additional gene alteration events or for specific use in different expression systems. For example, alternative comparable plant plasmids or integration vectors such as, e.g. those based on T-DNA, can be constructed for stable expression in plant cells according to the disclosures herein. Such constructs would use a plant specific promoter such as, e.g., cauliflower mosaic virus 35S promoter, to replace the promoters directing expression of the neo, hyg or aureobasidinA resistance gene disclosed herein, including for example, in Figures 7B, 9 and 10 herein. Moreover, the green fluorescent protein (GFP) sequence used herein may be modified to increase expression in plant cells such as Arabidopsis and the other plants disclosed herein as described in Haseloff et al., Proc. Natl. Acad. Sci. 94(6): 2122-7 (1997), Rouwendal et al. Plant Mol. Biol. 33(6): 989-99 (1997) and Hu et al. FEBS Lett. 369(2-3): 331-4 (1995). Codon usage for optimal expression of GFP in plants results from increasing the frequency of codons with a C or a G in the third position from 32 to about 60%. Specific constructs are disclosed and can be used as follows with such plant specific alterations.

We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137 \rightarrow G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHYGeGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer Hygrepr (5'GACCTATCCACGCCCTCC-3'), Hyg Δ r (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrefp (5'-CTGGGATAGGTCTGCGG-3'), Hyg Δ f

(5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGTCCCTGCGG-3'), respectively to primer HygEGFPr (5'-AAATCACGCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 µg of vector pHYGeGFP and 5 µg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHYGeGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

Oligonucleotide synthesis and cells. Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper et al., *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 µg/ml per A₂₆₀ unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*recA*).

Cell-free extracts. Although this portion of this example is directed to mammalian systems, similar extracts from plants can be prepared as disclosed elsewhere in this application and used as disclosed in this example. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately 2x10⁸ cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM MgCl₂; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000xg. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage.

We then immediately aliquote and freeze the supernatant at -80°C. We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C. We then centrifuge the cultures at 5000xg, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000xg for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000xg for 15 minutes. We then add glycerol to the clarified extract to a concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 µl are used, consisting of 10-30 µg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 µg chimeric double-hairpin oligonucleotide or 0.55 µg single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 µg of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM MgCl₂, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min.

The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 µl H₂O, and is stored at -20°C. 5 µl of plasmid from the resuspension (~100 ng) was transfected in 20 µl of DH10B cells by electroporation (400 V, 300 µF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 µg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 µl SOC. 200 µl is added undiluted to each of two kanamycin (50 µg/ml) agar plates and 200 µl of a 10⁵ dilution is added to an ampicillin (100 µg/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an AccuCount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10⁻⁵ to correct for the amp dilution.

The following procedure can also be used. 5 µl of resuspended reaction mixtures (total volume 50 µl) are used to transform 20 µl aliquots of electro-competent DH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50 µg/ml kanamycin or 12 µg/ml tetracycline is added for an additional 3 hours.

5 Prior to plating, the bacteria are pelleted and resuspended in 200 µl of SOC. 100 µl aliquots are plated onto kan or tet agar plates and 100 µl of a 10⁻⁴ dilution of the cultures are concurrently plated on agar plates containing 100 µg/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads.

Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies

10 are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

Chimeric single-stranded oligonucleotides. In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene.

Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan^s system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in

the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective 5 gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple 10 experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base 15 changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many 20 phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the exemplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines 25 indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

Correction of a mutant kanamycin gene in cultured mammalian cells. Although this portion of this example is directed to cultured mammalian cells, comparable methods may be used using cultured plant cells or protoplasts of those cells from the plant species disclosed herein. The experiments are performed using different eukaryotic cells including plant and mammalian cells, including, for example, 30 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO₂ in a humidified incubator to a density of 2 x 10⁵ cells/ml in an 8 chamber slide (Lab-Tek). After replacing the

regular DMEM with Optimem, the cells are co-transfected with 10 µg of plasmid pAURNeo(-)FIAsH and 5 µg of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10 µg lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan^s gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FIAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FIAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid pkan^sm4021 (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTetΔ208. Table 4 illustrates data from repair of the pkan^sm4021 point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan^r or tet^r and fold increases (single strand versus double hairpin) are presented for kan^r in Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion

activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold in certain embodiments when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK^sm4021 contains a mutation (T→G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan^s mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan^s mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

Frame shift mutations are repaired. By using plasmid pT^sΔ208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is

used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used.

Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides. From a comparison of molecules VII and XI, it is apparent that gene repair is more subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

Oligonucleotides can target multiple nucleotide alterations within the same template. The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK^sm4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence **TTCGATAAGCCTATGCTGACCCGTG** corrects the original mutation present in the kanamycin resistance gene of pK^sm4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence **TTCGGCTACGACTGGGCACAACAGACAATTGGC** with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK^sm4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK^sM4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-

TTGTGCCAGTC**G**TATCCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAG**C**ATTGTCTGTTGCCAGTC**G**TAGCCGAA

TAGCCTCTCCACCCAACGGCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-

5 GCTGACAGCCGGAACACGGCGGCATCAGAGCAG**C**ATTGTCTGTTGCCAGTC**G**TAGCCGAA
AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK⁸m4021 by monitoring kanamycin
10 resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to determine whether the additional, silent alteration has also been introduced. The results of an analysis
15 are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

20 *Nuclease sensitivity of unmodified DNA oligonucleotide.* Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

Plant extracts direct repair. The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract or extracts made from other plant cells disclosed herein. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl;

1.5 mM MgCl₂; 10 mM DTT; and 10% [v/v] glycerol). Some plant cell-free extracts also include about 1% (w/v) PVP. We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000 x g for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by
5 Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the
10 chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

Gene repair activity is directed by single-stranded oligonucleotides.

Oligonucleotide	Plasmid	Extract (ug)	kan' colonies	Fold increase
I	pK ^S m4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
I		20	0	
I		-	0	

Plasmid pK^Sm4021 (1 μ g), the indicated oligonucleotide (1.5 μ g chimeric oligonucleotide or 0.55 μ g single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20 μ g of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan' colonies counted. The data represent the number of kanamycin resistant colonies per 10⁶ ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan' colonies (second reaction) and in all reactions was calculated using the 20 μ g sample.

Table II

Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.

A. Oligonucleotide	Plasmid	Extract	kan ^r colonies
IX (3S/25G)		HUH7	637
X (6S/25G)		HUH7	836
IX		MEF2 ^{-/-}	781
X		MEF2 ^{-/-}	676
IX		MEF3 ^{-/-}	582
X		MEF3 ^{-/-}	530
IX		MEF ⁺⁺	332
X		MEF ⁺⁺	497
-		MEF2 ^{-/-}	10
-		MEF3 ^{-/-}	5
-		MEF ⁺⁺	14

Chimeric oligonucleotide (1.5 µg) or modified single-stranded oligonucleotide (0.55 µg) was incubated with 1µg of plasmid pK^m4021 and 20µg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 (2^{-/-}) or MSH3 (3^{-/-}) deleted. MEF⁺⁺ indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10⁶ ampicillin resistant colonies.

Table III

Frameshift mutation repair is directed by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	<i>tet</i> ^r colonies
Tet IX (3S/25A; 0.5 µg)	pT ^r Δ208 (1µg)	-	0
-	-	20µg	0
Tet IX (0.5 µg)	-	-	48
Tet IX (1.5 µg)	-	-	130
Tet IX (2.0 µg)	-	-	68
Tet I (chimera; 1.5 µg)	-	-	48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide.

The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of pT^rΔ208. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

Plant cell-free extracts support gene repair by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	kan' colonies
II (chimera)	pK ^S m4021	30µg Canola	337
IX (3S/25G)		Canola	763
X (6S/25G)		Canola	882
II		Musa	203
IX		Musa	343
X		Musa	746
-		Canola	0
-		Musa	0
IX		- Canola	0
X		- Musa	0

Canola or Musa cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 µg) and modified single-stranded oligonucleotides IX and X (0.55µg) were used to correct pK^Sm4021. Total number of kan' colonies are present per 10⁷ ampicillin resistant colonies and represent an average of four independent experiments.

Table V

*Gene repair activity in cell-free extracts prepared from yeast (*Saccharomyces cerevisiae*)*

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	kan' /amp' x 10 ⁶
Wild type	pKan'm4021	1 μ g	1 μ g	0.36
Wild type		1 μ g	1 μ g	0.81
Δ RAD52				10.72
Δ RAD52				17.41
Δ PMS1		1 μ g	1 μ g	2.02
Δ PMS1				3.23

In this experiment, the kan' gene in pKan'm4021 is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/2SG).

EXAMPLE 2
**Yeast Cell Targeting Assay Method for Base
Alteration and Preferred Oligonucleotide Selection**

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the 5 plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In 10 pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting 15 a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, 20 pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 µg pAUR123 vector DNA, as well 25 as, 10 µg of each pHyg(x)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to 30 support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74 α , is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence.

5 Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2'-O-methylated modified oligonucleotide may be used as a control. Alternatively, oligonucleotides containing one, two, three, four, five, six, eight, ten or more LNA modifications on at least one of the two termini (and preferably the 3' terminus) may be used in different embodiments.

10 *Oligonucleotide synthesis and cells.* We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 MAT α at low copy number under aureobasidin selection.

15 Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD₆₀₀ was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml

20 ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 μ l 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 μ l of cells with 5 μ g of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes.

25 We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 μ F, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300

rpm for 6 hours. We then spread 200 μ l of this culture on selective plates containing 300 μ g/ml hygromycin and spread 200 μ l of a 10⁵ dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number 30 of hygromycin resistance colonies per 10⁵ aureobasidinA resistant colonies.

Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells

containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction
5 activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide
10 (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-
15 CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGGTAC**GTCCTGCGGGTAAATAGCTGCGCCGATG**
GTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-
CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGGATAACGT**CCTGCGGGTAAACAGCTGCGCCGATG**
GTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-
20 CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGGATAACGT**CCTGCGGGTAAATAGCTGCGCCGACG**
GTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

Oligonucleotides targeting the sense strand direct gene correction more efficiently. We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 25 7 and 8, indicate that an oligonucleotide, HygE3T/74 α , with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide
30 concentrations from 0-3.6 μ g, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74 α and HygE3T/74).

Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74 α relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

Optimization of oligonucleotide concentration. To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74 α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74 α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0 μ g. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in pAURHYG(ins)GFP by HygGG/Rev, HygE3T/25 and HygE3T/74

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10 ⁵)	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μ g)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74 α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

Correction of a base substitution mutation is more efficient than correction of a frame-shift mutation.

Oligonucleotide Tested (5 µg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

Table 9

Optimization of oligonucleotide concentration in electroporated yeast cells.

Amount (µg)	Colonies on hygromycin	Colonies on aureobasidin (/10 ⁵)	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

Example 3 Cultured Cell Manipulation

Although disclosure in this example is directed to use of stem cells or human blood cells and microinjection, the microinjection procedures may also be used with cultured plant cells or protoplasts using any plant species, including those disclosed herein. Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either

the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). Lin⁻CD38⁻ cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA). Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection.

5 S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 µg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 µg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM (Stem Cell Technologies), 40 µg/ml low-density lipoprotein (LDL; Sigma, St. Louis, MO), 50 mM HEPES buffer and 50 µM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After 10 microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

15 35 mm dishes are coated overnight at 4° C with 50 µg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 µm to 0.3 µm outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are fluorescently labeled allow determination of the amount of 20 oligonucleotide delivered to the cells.

For *in vitro* erythropoiesis from Lin⁻CD38⁻ cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythroid progeny. CD34+ cells can convert a normal A (β^A) to sickle T (β^S) mutation in the β -globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

30 Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids,

liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

Biolistic delivery of oligonucleotide into plant cells may be accomplished according to the following method. One milliliter of packed cell volume of plant cell suspensions are subcultured onto plates containing solid medium [with Murashige and Skoog salts from Gibco/BRL, 500 mg/liter Mes, 1 mg/liter thiamin, 100 mg/liter myo-inositol, 180 mg/liter KH₂PO₄, 2.21 mg/liter 2,4-dichlorophenoxyacetic acid (2,4-D), and 30 g/liter sucrose (pH 5.7) and having 8 g/liter agar-agar from Sigma added before autoclaving]. By using a helium-driven particle gun such as that from BioRad and following manufacturers directions, oligonucleotides may be introduced to cells after precipitation onto 1 micrometer or comparable gold microcarriers (Bio-Rad). To precipitate onto microcarriers, 35 microliters of a particle suspension (60 mg of microcarriers per ml of 100% ethanol) is transferred to a 1.5 ml microcentrifuge tube, which is agitated on a vortex mixer. Then 40 microliter of resuspended oligonucleotide (60 ng/microliter water) is added; then 75 microliter of ice-cold 2.5 M CaCl₂ is added; then 75 microliter of ice-cold 0.1 M spermidine is added. The tube is mixed vigorously or a vortex mixer for 10 min at room temperature. The particles are allowed to settle for 10 min and are centrifuged at 11,750 g for 30 sec. The supernatant is removed and the particles are resuspended in 50 microliter of 100% ethanol. An aliquot of 10 microliter of the resuspended particles are applied to each macro-projectile which is used to bombard each plate once at 900 psi (1 psi = 6.89 kPa) with a gap distance (distance from power source to macroprojectile) of 1 cm and a target distance (distance from microprojectile launch site to target material) of 10 cm.

An alternative method of delivery can be used as follows. Cultured cells are suspended in liquid N6 medium and then plated on a VWR Scientific glass fiber filter. About 0.4 microgram of oligonucleotide are precipitated with 15 microliter of 2.5 mM CaCl₂ and 5 microliter of 0.1 M spermidine onto 25 microgram of 1.0 micrometer gold particles. Microprojectile bombardment is performed by using a Bio-Rad PDS-1000 He particle delivery system or comparable machine following manufacturers instructions. Alterations in oligonucleotide concentrations can be employed to determine the optimum concentration of oligonucleotide according to the procedures described herein for any particular oligonucleotide of the invention.

Alternatively, the oligonucleotide of the invention may be delivered to a plant cell by electroporation of a protoplast derived from a plant part. The protoplasts may be formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques such as those in Gallois et al., Methods in Molecular Biology 55: 89-107 by Humana Press. Such conditions for electroporation use

about 3×10^5 protoplasts in a total volume of about 0.3 ml with a concentration of oligonucleotide of between 0.6 to 4 microgram per ml.

EXAMPLE 4

Plant Cells

5 The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific 10 site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon

. Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations 15 can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

For introduction of a T-DNA, including the T-DNA in the plasmid of Figure 11, into a plant cell, *Agrobacterium tumefaciens* is used. These techniques are routine standard techniques known in the art. For example, one method follows. We transform *A. tumefaciens* is transformed by electroporation (using a BioRad Gene Pulser™). Competent *A. tumefaciens* is prepared using a method similar to that of preparing competent *E. coli* by suspending a freshly grown culture three times in ice-cold water and a final resuspension in 10% glycerol. Electroporation conditions are a 0.2 cm gap cuvette at a setting of 25 20 μ F, 200 Ω and 2.5 kV.

A. tumefaciens containing a plasmid with a T-DNA is then used to introduce the T-DNA into a plant cell using routine standard techniques known in the art. For example, we transform 25 *Arabidopsis* by vacuum infiltration or by dipping flowers in an Agrobacterium solution containing a surfactant, e.g. L-77. Seeds are then collected, grown and screened for presence of the T-DNA. Alternatively, Agrobacterium can be used to transform callus tissue and the callus tissue can then be used to regenerate transformed plants.

All publications and patent applications cited in this specification are herein incorporated 30 by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some

detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

5 **Notes on the tables presented below:**

Each of the following tables presents, for the specified gene, a plurality of mutations that are known to confer a relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the genome according to the present invention.

10 The left-most column identifies each alteration or mutation and the phenotype that the alteration/mutation confers.

15 For most entries, the mutation/alteration is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

20 The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the genome or in cloned DNA including DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

25 All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

30 The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair/altering nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair/alteration. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair/alteration nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

Example 5**Engineering herbicide resistant plants**

Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

Table 10
Genome-Altering Oligos Conferring Glyphosate Resistance

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Glyphosate Resistance EPSPS <i>Arabidopsis thaliana</i> Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTTCTGCCTCCAAGTCTCTATCAAATCGGATCCTGC TTCTCGCTGCTCTGCTGAGGTATATCAC	4341
		GTGATATATACTCAGACAGAGCAGCGAGAAGCAGGATCCGATT TGATAGAGACTTGGAGGCAGGAAGCTTAATAAGACCGGAGATT CTCTAATGGGTTGAAGTACAATCTCGACGCTT	4342
		GCTTCCTGCCTCCAAGT	4343
		ACTTGGAGGCAGGAAGC	4344
10	Glyphosate Resistance EPSPS <i>Brassica napus</i> Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTCAACCAATCAGAGAAATCTCGGGTC TCATTAAGCTACCCGATCCAAATCTCTCCAATCGGATCCTCC TTCTTGCGCGCTCTATCTGAGGTACATATACT	4345
		AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT GGAGAGAGATTGGATGCGGGTAGCTTAATGAGACCCGAGATT CTCTGATTGGGTTGAAGCACAATCTCTGAAGCTT	4346
		GCTACCCGATCCAAAT	4347
		ATTTGGATGCGGGTAGC	4348
		AGCCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC ACTGTTAAATTGCCTGCTTCTAAATCCCTTCCAATCGTATTCTCC TTCTTGCTGCCCTTCTAAGGGAAAGGACTGT	4349
15	Glyphosate Resistance EPSPS 1 <i>Nicotiana tabacum</i> Gly95Ala GGT-GCT	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAACGATT GGAAAGGGATTAGAACAGGCAATTAAACAGTGCCCTGATATATC TTTGATGGGTTGCAGCACAATCTGTTGGGCT	4350
		ATTGCCTGCTTCTAAAT	4351
		ATTAGAACAGGCAAT	4352
		ATTGTTTCTTGGTACGAAATGCTCCTGTTGCAATTGTCAGCA AGGGAGGCCCTCCCGCAGGGAAAGGTAAAGCTCTGGATCAATT AGCAGCCAGTACTGACTGCTCTGCTTATGGC	4353
		GCCATAAGCAGAGCAGTCAGTCAAGTACTGGCTGCTAATTGATCCAGA GAGCTTACCTCCCTGCGGGAAAGGCCCTCCCTGCTGACAATT GAACAGGAGGACATTTCGTACCAAGGAAACAAT	4354
20	Glyphosate Resistance EPSPS 2 <i>Nicotiana tabacum</i> Gly62Ala GGA-GCA	CCTCCCCGAGGGAGG	4355
		CCTTCCCTGCGGGAGG	4356
		ATTGTTTCTTGGCACTGACTGCCACCTGTTGTCATGGAA TCGGAGGGCTACCTGCTGGCAAGGTCAAGCTGCTGGCTCCATC AGCAGTCAGTACTTGAGTGCCCTGCTGATGGC	4357
		GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA CAGCTTGACCTGCCAGCAGGTAGCCCTCCGATTCCATTGACAC GAACAGGGGGCAGTCAGTGCCAGGAAACAAT	4358
25	Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT		
30	Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCTACCT <u>G</u> TGGCAAGG	4359
	CCTTGCC <u>A</u> G <u>C</u> AGGTAGC	4360
5 Glyphosate Resistance EPSPS <i>Oryza sativa</i> Gly115Ala GGT-GCT	ACTGTTCC <u>T</u> GGCACTGAATGCCAAC <u>T</u> GTC <u>G</u> TCAAGGGAA ATTGGAGGA <u>C</u> TT <u>C</u> TC <u>G</u> T <u>C</u> GGCAAGGTTAAGCTCTGGTTCCAT CAGCAGTCAGTACTTGAGTGCTGC <u>T</u> GATGGC GCCATCAGCAAGGCA <u>T</u> CTCAAGTACTGACTGCTGATGGAA <u>C</u> AGA GAGCTTAAC <u>C</u> TTGCC <u>C</u> AGCAGGAAGTC <u>C</u> CCAATT <u>C</u> CC <u>T</u> GACAC GAACAGGTGGG <u>C</u> ATT <u>C</u> AGT <u>G</u> CCAAGGAA <u>A</u> AGT ACTTC <u>C</u> T <u>G</u> TGGCAAGG	4361 4362 4363 4364
10 Glyphosate Resistance EPSPS <i>Petunia x hybrida</i> Gly93Ala GGC-GCC	AGCCTTCTGAGATAGTGTGCAACCCATTAAAGAGAT <u>T</u> CAGGCA CTGTTAAATTGCCT <u>G</u> C <u>C</u> CTCTAA <u>T</u> ATT <u>C</u> ATT <u>T</u> CTAA <u>T</u> AGAATT <u>C</u> C <u>T</u> TCTTGCTGC <u>C</u> TT <u>T</u> CTGAAGGAA <u>C</u> ACTGT ACAGTT <u>G</u> CC <u>T</u> TC <u>C</u> AGATAAGGCA <u>G</u> AG <u>A</u> AGG <u>G</u> AA <u>T</u> TC <u>T</u> ATT <u>A</u> GATAAT <u>G</u> ATT <u>T</u> AG <u>G</u> GC <u>AG</u> GA <u>AT</u> TAACAGTGCCTGAA <u>A</u> CT TTAATGGGTGCAAC <u>A</u> CT <u>T</u> CT <u>C</u> AGAAGGCT ATTGCCT <u>G</u> C <u>C</u> CT <u>T</u> AA <u>A</u> AT AT <u>T</u> TA <u>G</u> AG <u>G</u> GC <u>AG</u> GA <u>AT</u> AT	4365 4366 4367 4368
15 Glyphosate Resistance EPSPS <i>Lycopersicon esculentum</i> Gly97Ala GGT-GCT	AACCCC <u>T</u> GAGAT <u>T</u> GTGCTAGNACCC <u>C</u> ATCAA <u>A</u> GA <u>T</u> AT <u>T</u> CTGG <u>T</u> A CTGTTAA <u>A</u> TT <u>A</u> CC <u>C</u> CG <u>T</u> CG <u>A</u> AT <u>C</u> C <u>T</u> TT <u>C</u> CA <u>A</u> TC <u>G</u> T <u>A</u> TT <u>C</u> C <u>T</u> TCTTGCTGC <u>C</u> CT <u>T</u> CT <u>T</u> GT <u>G</u> AG <u>G</u> GA <u>AG</u> GT <u>C</u> T ACAGTC <u>C</u> TT <u>C</u> C <u>T</u> CA <u>G</u> AA <u>A</u> GG <u>G</u> CA <u>G</u> CA <u>A</u> AG <u>G</u> GA <u>A</u> AC <u>G</u> ATT GGAA <u>A</u> GG <u>G</u> AT <u>T</u> CG <u>A</u> AG <u>C</u> GG <u>G</u> TA <u>A</u> TT <u>A</u> AC <u>G</u> T <u>AC</u> CA <u>U</u> AT <u>T</u> C <u>A</u> T <u>GG</u> TT TTTGATGGGTNCTAGCACA <u>A</u> CT <u>T</u> C <u>A</u> T <u>GG</u> TT ATTACCC <u>C</u> CG <u>T</u> CG <u>A</u> AT AT <u>T</u> TC <u>G</u> AA <u>G</u> CG <u>GG</u> TA <u>A</u> AT	4369 4370 4371 4372
20 Glyphosate Resistance EPSPS <i>Lolium rigidum</i> Gly107Ala GGT-GCT	ATTGTTCC <u>T</u> GGCACTGACTGCCAAC <u>T</u> GTC <u>G</u> KATCAACGGCA TTGGAGGG <u>C</u> TAC <u>C</u> T <u>G</u> T <u>C</u> GGCAAGGTTAAGCTGT <u>T</u> GG <u>T</u> CC <u>A</u> TC AGCAG <u>C</u> CA <u>A</u> ACT <u>T</u> GT <u>G</u> AG <u>T</u> CC <u>T</u> GT <u>G</u> T <u>A</u> GGC GCCATCAGCAAG <u>G</u> AA <u>C</u> TC <u>A</u> GT <u>T</u> GG <u>C</u> T <u>G</u> T <u>A</u> GGAA <u>C</u> AGA CAGCTTAAC <u>C</u> TTGCC <u>C</u> AG <u>C</u> AG <u>G</u> T <u>A</u> GG <u>C</u> CC <u>T</u> CA <u>A</u> T <u>G</u> CC <u>T</u> GT <u>A</u> CG AACAGGTGGG <u>C</u> AG <u>T</u> GT <u>G</u> CCA <u>A</u> GG <u>A</u> AC <u>A</u> AT GCTACCT <u>G</u> TGGCAAGG	4373 4374 4375 4376

Table 11
Genome-Altering Oligos Conferring Imidazolinone and Sulfonlurea Herbicide Resistance

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Sulfonlurea Resistance ALS	AGCGGATTAGCCGATGC GTT TAGATAGTGT CCT CTT TAGCA ATCACAGGACAAGTC <u>T</u> CTCGTGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAAACGCGTT	4377
10	<i>Arabidopsis thaliana</i> Pro197Ser CCT-TCT	AACCGCTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGAGAGACTTGTCTGTGATTGCTACAAGAGGAA	4378
		CACTATCTAACAAACGCATCGGCTAACCGCT	4379
		GACAAGT <u>C</u> TCGTCGT	4380
		ACGACGAGAGACTTGTC	
15	<i>Arabidopsis thaliana</i> Pro197Gln CCT-CAG	AGCGGATTAGCCGATGC GTT TAGATAGTGT CCT CTT TAGCA ATCACAGGACAAGTC <u>C</u> AGCGTGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAAACGCGTT	4381
		AACCGCTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACG <u>T</u> GGACTTGTCTGTGATTGCTACAAGAGGAA	4382
		CACTATCTAACAAACGCATCGGCTAACCGCT	4383
		ACAAGT <u>C</u> AGCGTCGT	4384
		TACGACG <u>T</u> GGACTTGT	
20	<i>Arabidopsis thaliana</i> Pro197Gln CCT-CAA	AGCGGATTAGCCGATGC GTT TAGATAGTGT CCT CTT TAGCA ATCACAGGACAAGTC <u>C</u> AACGTGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAAACGCGTT	4385
		AACCGCTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACG <u>T</u> GGACTTGTCTGTGATTGCTACAAGAGGAA	4386
		CACTATCTAACAAACGCATCGGCTAACCGCT	4387
		ACAAGT <u>C</u> AACGTGT	4388
		TACGACG <u>T</u> GGACTTGT	
25	<i>Arabidopsis thaliana</i> Ser653Asn AGT-AAC	GACCTTACCTGTTGATGTGATTTGTCCGCCACCAAGAACATGTGT TGCGGATGATCCC <u>G</u> ACGGTGGCACTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4389
		ATCTCTCAGTATTTAATCCGGCCATCTCCTCCGTATGACATCGT TGAAAGTGCCACC <u>G</u> TCGGGATCATCGGCAACACATGTTCTGGT GCGGACAAATCACATCCAACAGGTAAAGGT	4390
		GATCCC <u>G</u> AACGGTGGCA	4391
		TGCCACC <u>G</u> TCGGGATC	4392

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTGTCCGCACCAAGAACATGTGT TGCCGATGATCCC <u>GAATGGTGGC</u> ACTTCAACGATGTCTAACCGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4393
		ATCTCTAGTATTAATCCGGCCATCTCCCTCCGTATGACATCGT TGAAA <u>GTGCCACCATT</u> CGGGATCATCGGCAACACATGTTCTGGT GCGGACAAATCACATCCAACAGGTAAAGGTC	4394
		GATCCC <u>GAATGGTGGC</u> A	4395
		TGCCACC <u>ATT</u> CGGGATC	4396
		TCCCGCGCTCGCCGACCGCGCTGCTCGACTCCGTCGGATGGTCG CCATCACGGGCCAGGTCT <u>CCCCCGCG</u> CATGATGGCACCGACGC CTTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4397
10	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	AGCGGGTGACCTCGACTATGGCGTCTCCTGGAAAGGCGTCGGT CCGATCATGCGCGGG <u>AGAC</u> CTGGCCCGTATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4398
		GCCAGGT <u>CTCCCCGCGC</u>	4399
		GC <u>GGCGGGAGAC</u> CTGGC	4400
		CCCGCGCTCGCCGACCGCGCTGCTCGACTCCGTCGGATGGTCGC CATCACGGGCCAGGT <u>CCAAACGCCG</u> CATGATGGCACCGACGCC TTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4401
		GAGCGGGTGACCTCGACTATGGCGTCTCCTGGAAAGGCGTCGGT GCCGATCATGCGCG <u>CTGG</u> ACCTGGCCCGTATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4402
15	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	CCAGGT <u>CCAAACGCCG</u> CA	4403
		T <u>GC</u> GGCG <u>CTGG</u> ACCTGG	4404
		CCCGCGCTCGCCGACCGCGCTGCTCGACTCCGTCGGATGGTCGC CATCACGGGCCAGGT <u>CCAGCGCCG</u> CATGATGGCACCGACGCC TTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4405
		GAGCGGGTGACCTCGACTATGGCGTCTCCTGGAAAGGCGTCGGT GCCGATCATGCGCG <u>CTGG</u> ACCTGGCCCGTATGGCGACCATCG GGGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4406
		CCAGGT <u>CCAGCGCCG</u> CA	4407
20	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	T <u>GC</u> GGCG <u>CTGG</u> ACCTGG	4408
		GGCCATACTTGTGGATATCATCGTCCCGACCAAGGAGCATGTGC TGCCTATGATCCC <u>AAATGGGGCG</u> CATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4409
		ATAGATTAATACACAGTCCTGCCATACCCATCCAGGATCATGTCCT TGAATGCGCCCC <u>CAATTGGG</u> ATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATCCAACAAGTATGCC	4410
		GATCCC <u>AAATGGGGCG</u>	4411
25	Imidazolinone Resistance ALS <i>Oryza sativa</i> Ile627Asn ATT-AAT		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	CGCCCCCATTTGGGATC	4412
		TCCCGCGCTCGCCGACGCCGCTCGACTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCC TCCAGGAGACGCCATCGTCGAGGTACCCGCT	4413
		AGCGGGTGACCTCGACGATGGCGTCTCTGGAAAGGCGTCGGT GCCAATCATGCGTCGCGACACCTGTCCCGTATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4414
		GACAGGTGTCGCGACGC	4415
		GCGTCGCGACACCTGTC	4416
	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CCCGCGCTCGCCGACGCCGCTCGACTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGCAAGCGACGCATGATTGGCACCGACGCC CCAGGAGACGCCATCGTCGAGGTACCCGCTC	4417
10		GAGCGGGTGACCTCGACGATGGCGTCTCTGGAAAGGCGTCGG TGCCAATCATGCGTCGCTGCACCTGTCCCGTATGGCGACCATGG GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4418
		ACAGGTGCAAGCGACGC	4419
		TGCGTCGCTGCACCTGT	4420
	Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	GGCCGTACCTCTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAATGGTGGGCTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4421
		TTAGATCAGTACACAGTCCTGCCATACCACCCAGGATCATATCCT TGAAAGCCCCACCCATTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4422
15		GATCCCTAATGGTGGGG	4423
		CCCCACCAATTAGGGATC	4424
	Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAC	GGCCGTACCTCTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAACGGTGGGCTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4425
		TTAGATCAGTACACAGTCCTGCCATACCACCCAGGATCATATCCT TGAAAGCCCCACCGTTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4426
		GATCCCTAACGGTGGGG	4427
20		CCCCACCGTTAGGGATC	4428
	Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Ser CCG-TCG	TCCCGCGCTCGCCGACGCCCTCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTCTCGCGCCGCATGATGGCACGGACGCC TTCCAGGAGACGCCATCGTCGAGGTACCCGCT	4429
		AGCGGGTGACCTCGACGATGGCGTCTCTGGAAAGGCGTCGGT GCCGATCATGCGCGCGAGACCTGCCCCGTATGGCCACCATGG GGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	4430

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Gln CCG-CAG	GGCAGGT <u>C</u> CGCGCCGC	4431
		GCGGCGCG <u>A</u> GACCTGCC	4432
		CCGCGCTCGCCGACGCCCTCCTGACTCCATCCCCATGGTGGCC ATCACGGGGCAGGT <u>C</u> ACGCCGCATGATGGCACGGACGCC TCCAGGAGACGCCATCGTCGAGGTACCCGCTC	4433
		GAGCGGGTGACCTCGACGATGGCGTCTCTGGAAAGGCGTCCG TGCCGATCATGCGGCCG <u>T</u> GGACCTGGCCCGTGTGGCCACCATG GGGATGGAGTCGAGGGAGGGCGTCGGCAGCGCGG	4434
		GCAGGT <u>C</u> ACGCCGC	4435
		TGCGGCGC <u>T</u> GGACCTGC	4436
	Imidazolinone Resistance ALS <i>Lolium multiflorum</i> Ser623Asn AGC-AAC	CTGGGCCATA <u>T</u> GTGGATATCATCGTCCCTCACCAAGGAGCATG TGCTGCCTATGATCC <u>T</u> ACGGTGGTGCTTCAAGGACATTATCA TGGAAAGGTGATGGCAGGATT <u>T</u> CGTATTAAAC	4437
		GT <u>T</u> TAATACGAA <u>T</u> CTGCCATCAC <u>T</u> TCATGATA <u>A</u> TGTCC <u>T</u> GA AAGCACCA <u>C</u> CG <u>T</u> AGGGATCATAGGCAGCACATGCTCCTGGTGA GGGACGATGATATCCAACAAGTATGGCCAG	4438
		GATCC <u>C</u> TA <u>A</u> CGGTGGT	4439
		CACCACCG <u>T</u> AGGGATC	4440
10	Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Ser CCA-TCA	TC <u>C</u> CGCGCTCGCCGACGCTCTCCTGACTCCATCCCCATGGTGC CATCACGGGC <u>C</u> AGGT <u>T</u> CACGCCGCATGATGGCACGGACGCC TCCAGGAGACGCCATAGTGGAGGTACCGC	4441
		AGCGCGTGACCTCCACTATGGCGTCTCCTGGAACCGCGTCCGT CCGATCATGCGGCCG <u>T</u> AGACCTGGCCCGTGTGGCACCATGG GGATGGAGTCGAGGGAGAGCGTCGGCAGCGCGGA	4442
		GCCAGGT <u>C</u> TCACGCCGC	4443
		CGGGCGTG <u>A</u> GACCTGGC	4444
15	Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Gln CCA-CAA	CCGCGCTCGCCGACGCTCTCCTGACTCCATCCCCATGGTGC ATCACGGGC <u>C</u> AGGT <u>T</u> CACGCCGCATGATGGCACGGACGCC CCAGGAGACGCCATAGTGGAGGTACCGC	4445
		GAGCGCGTGACCTCCACTATGGCGTCTCCTGGAACCGCGTCCGT GCCGATCATGCGGCCG <u>T</u> GGACCTGGCCCGTGTGGCACCATGG GGATGGAGTCGAGGGAGAGCGTCGGCAGCGCGGA	4446
		CCAGGT <u>C</u> ACGCCGC	4447
		TGCGGCG <u>T</u> GGACCTGG	4448

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Imidazolinone Resistance ALS <i>Hordeum vulgare</i> Ser524Asn AGC-AAC	CCCAAGGGCCGTACCTGCTGGATATCATTGTCCCCCATCAGGAGC ACGTGCTGCCTATGATCCC <u>A</u> CGGTGGTGTTCAGGACATGA TCATGGAGGGTGATGGCAGGACCTCGTACTGA	4449
		TCAGTACGAGGTCTGCCATCACCCCATGATCATGTCCTGAA AGCACCAACC <u>G</u> GGATCATAGGCAGCACGTGCTCCTGATGCG GGACAATGATATCCAGCAGGTACGGCCCTGGG	4450
		GATCCC <u>A</u> CGGTGGT	4451
		CACCACCG <u>T</u> GGGATC	4452
10	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTC <u>T</u> CTCGTCGGATGATCGGTACCGATGCTTC CAGGAAACTCCAATTGTTGAGGTAAACAAGGT	4453
		ACCTTGTACCTCAACAATTGGAGTTCTGGAAAGCATCGGTAC CGATCATCCGACGAG <u>G</u> ACTTGACCAGTGTGACCAGTACGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4454
		GTCAAGTC <u>T</u> CTCGTCGG	4455
		CCGACGAG <u>G</u> ACTTGAC	4456
		GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTC <u>A</u> CGTCGGATGATCGGTACCGATGCTTC AGGAAACTCCAATTGTTGAGGTAAACAAGGT	4457
15	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GACCTTGTACCTCAACAATTGGAGTTCTGGAAAGCATCGGTAC CCGATCATCCGACG <u>G</u> GTGGACTTGACCAGTGTGACCAGTACGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCACT	4458
		TCAAGTC <u>C</u> ACGTGGGA	4459
		TCCGACG <u>G</u> GTGGACTTGA	4460
		GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTC <u>C</u> AGCGTCGGATGATCGGTACCGATGCTTC AGGAAACTCCAATTGTTGAGGTAAACAAGGT	4461
		GACCTTGTACCTCAACAATTGGAGTTCTGGAAAGCATCGGTAC CCGATCATCCGACG <u>G</u> CTGGACTTGACCAGTGTGACCAGTACGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCACT	4462
20	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	TCAAGTC <u>C</u> AGCGTCGGAA	4463
		TCCGACG <u>G</u> CTGGACTTGA	4464
		GACCTTAC <u>T</u> GTGGATGTGATTGTCCCCACATCAAGAACATGTCCT GCCTATGATCCC <u>A</u> GGAGGCGCTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATTGACCTCA	4465
		TGAGGTCAATATTGTGTTCTCCATCACCC <u>T</u> GTGATCACATCTT TGAAAGCCCTCC <u>A</u> GGGGATCATAGGCAGGACATGTTCTGAT GTGGGACAATCACATCCAACAAGTAAGGT	4466
		GATCCC <u>A</u> GGAGGCG	4467
25	Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		CGCCTCCATTGGGGATC	4468
5	Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACITCTGACTCAGTCCTCTTGTGCC TTACTGGGCAAGTT <u>CCCCGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTA <u>ACTCGAT</u> C	4469
		ATCGAGTTACCTAACAA <u>TTGGAGT</u> CTCTTGAAAAGCATCAGTACC AATCATACGCCGG <u>AAACT</u> TTGCCAGTA <u>ATGGCGACAAGAGGGA</u> CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4470
		GGCAAGTT <u>CCCCGGCGT</u>	4471
		ACGCCGG <u>AAACT</u> TGCC	4472
		CTGGTCTTGCTGATGCACITCTGACTCAGTCCTCTTGTGCCA TTACTGGGCAAGTT <u>CAACGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTA <u>ACTCGATC</u>	4473
10	Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAA	GATCGAGTTACCTAACAA <u>TTGGAGT</u> CTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>TTGA</u> ACTTGCCAGTA <u>ATGGCGACAAGAGGGA</u> CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4474
		GCAAGTT <u>CAACGGCGTA</u>	4475
		TACGCCG <u>TTGA</u> ACTTGC	4476
		CTGGTCTTGCTGATGCACITCTGACTCAGTCCTCTTGTGCCA TTACTGGGCAAGTT <u>CAGCGGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTA <u>ACTCGATC</u>	4477
		GATCGAGTTACCTAACAA <u>TTGGAGT</u> CTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>CTGA</u> ACTTGCCAGTA <u>ATGGCGACAAGAGGGA</u> ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4478
15	Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAG	GCAAGTT <u>CAGCGGGCGTA</u>	4479
		TACGCCG <u>CTGA</u> ACTTGC	4480
		GACCGTATCTGCTGGATGTAATCGTACCA <u>CAGGAGCATGTGC</u> TGCCTATGATCCCT <u>AACGGTGCCGCC</u> TTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4481
		ACCAACTAATAAGCCCTTCTTCATACC <u>CTGT</u> ATGGTGTCC TGAAGGGCGGCACCG <u>TTAGGGATC</u> AGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATA <u>CGGTC</u>	4482
		GATCCCT <u>AACGGTGCCG</u>	4483
25	Imidazolinone Resistance ALS <i>Amaranthus retroflexus</i> Ser652Asn AGC-AAC	CGGCACCG <u>TTAGGGATC</u>	4484

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Ser CCA-TCA	AGCGGCCTCGCTGACCGCCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGT <u>G</u> CACGTAGGATGATAGGTACTGATGCTTT CAGGAAACTCCTATTGTTGAGGTAACTAGAT	4485
		ATCTAGTTACCTCAACAATAGGAGTTCTGAAAAGCATCAGTACC TATCATCCTACGT <u>G</u> ACACTTGACCTGTTAGCAACAATGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4486
		GTCAAGT <u>G</u> T <u>C</u> ACGTAGG	4487
		CCTACGT <u>G</u> ACACTTGAC	4488
10	Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Gln CCA-CAA	GCAGGCCTCGCTGACCGCCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGT <u>G</u> CACGTAGGATGATAGGTACTGATGCTTT CAGGAAACTCCTATTGTTGAGGTAACTAGATC	4489
		GATCTAGTTACCTCAACAATAGGAGTTCTGAAAAGCATCAGTAC CTATCATCCTACGT <u>G</u> CACTTGACCTGTTAGCAACAATGGGA CGCTATCCAGTAGCGCGTCAGCGAGGCCG	4490
		TCAAGT <u>G</u> CACGTAGGA	4491
		TCCTACGT <u>G</u> CACTTGAC	4492
15	Imidazolinone Resistance ALS 1 <i>Nicotiana tabacum</i> Ser650Asn AGT-AAT	GGCCATACTTGGATGTGATTGTACCTCATCAGGAACATGTTT ACCTATGATTCCCA <u>A</u> TGGCGGAGCTTCAAAGATGTGATCACAGA GGGTGACGGGAGAA <u>G</u> TTCTATTGAGTTG	4493
		CAAAC ^T CAATAGGA <u>A</u> TTCTCCCGTACCCCTGTGATCACATCTT TGAAAGCTCCGCC <u>A</u> TTGGGAATCATAGGTAAAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4494
		GATTCCC <u>A</u> TTGGCGGAG	4495
		CTCCGCC <u>A</u> TTGGGAATC	4496
20	Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACC <u>G</u> GTCAAGT <u>G</u> CACGTAGGATGATCGGTACTGATGCTTT CAGGAAACTCCGATTGTTGAGGTAACTAGAT	4497
		ATCTAGTTACCTCAACAATCGGAGTTCTGAAAAGCATCAGTACC GATCATCCTACGT <u>G</u> ACACTTGACCGGTTAGCAACAATGGGAC GCTATCCAGTAGGGCGTCCCGAGGCCACT	4498
		GTCAAGT <u>G</u> T <u>C</u> ACGTAGG	4499
		CCTACGT <u>G</u> ACACTTGAC	4500
25	Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACC <u>G</u> GTCAAGT <u>G</u> CACGTAGGATGATCGGTACTGATGCTTT CAGGAAACTCCGATTGTTGAGGTAACTAGATC	4501
		GATCTAGTTACCTCAACAATCGGAGTTCTGAAAAGCATCAGTAC CGATCATCCTACGT <u>G</u> CACTTGACCGGTTAGCAACAATGGGA CGCTATCCAGTAGGGCGTCCCGAGGCCAC	4502
		TCAAGT <u>G</u> CACGTAGGA	4503

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		TCCTACGT <u>T</u> GCACTTGA	4504
5	Imidazolinone Resistance ALS 2 <i>Nicotiana tabacum</i> Ser647Asn AGT-AAT	GGCCATACTTGTGGATGTGATTGTACCTCATCAGGAACATGTTCTACCTATGATCCC <u>A</u> TGGCGGGGTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAACGTTCTATTGACTTTG	4505
		CAAAGTCATAGGAAC <u>T</u> CTCCCGTCACCCCTGTGATCACATCTT TGAAAGCCCCGCC <u>A</u> TGGGAATCATAGGTAGAACATGTTCTGATGAGGTACAATCACATCCAACAAAGTATGGCC	4506
		GATTCCC <u>A</u> TGGCGGGG	4507
		CCCCGCC <u>A</u> TGGGAATC	4508
10	Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Ser CCC-TCC	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTCCAATGGTTGCTA TTACTGGTCAAGTT <u>C</u> CCAGGAGAACATGATTGAAACAGATGCGTTCA AGAAACCCCTATTGTTGAGGTAAACACGTT	4509
		AACGTGTTACCTCAACAATAGGGTTCTTGAAACGCATCTGTTCC AATCATTCTCCTGG <u>A</u> ACTGACCAGTAATAGCAACCATTGGAACA CTGTCTAATAAAGCATCAGCAAGACCAC	4510
		GTCAAGTT <u>C</u> CCAGGAGA	4511
		TCTCCTGG <u>A</u> ACTTGAC	4512
		GTGGTCTTGCTGATGCTTTATTAGACAGTGTCCAATGGTTGCTAT TACTGGTCAAGTT <u>C</u> AGGAGAACATGATTGAAACAGATGCGTTCA AGAAACCCCTATTGTTGAGGTAAACACGTT	4513
15	Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAA	GAACGTGTTACCTCAACAATAGGGTTCTTGAAACGCATCTGTTCC CAATCATTCTCCT <u>T</u> GAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4514
		TCAAGTT <u>C</u> AAAGGAGAA	4515
		TTCTCCT <u>T</u> GAACTTGA	4516
		GTGGTCTTGCTGATGCTTTATTAGACAGTGTCCAATGGTTGCTAT TACTGGTCAAGTT <u>C</u> AGGAGAACATGATTGAAACAGATGCGTTCA AGAAACCCCTATTGTTGAGGTAAACACGTT	4517
		GAACGTGTTACCTCAACAATAGGGTTCTTGAAACGCATCTGTTCC CAATCATTCTCCT <u>T</u> GAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4518
20	Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAG	TCAAGTT <u>C</u> AGAGGAGAA	4519
		TTCTCCT <u>T</u> GAACTTGA	4520
		GGGCCTTACTTGTGGATGTGATCGTGC <u>CCC</u> CATCAAGAACATGTG TTGCCCATGATCCC <u>A</u> ATGGTGAGGTTCATGGATGTGATCACCGAAGGGCGACGGCAGAACATGAAATTGAGCTT	4521
		AAGCTCAATATTCTATTCTGCCCGCCTCGGTGATCACATCCAT GAAACCTCCACCA <u>T</u> CGGGATCATGGGCAACACATGTTCTGATGGGCACGATCACATCCAACAAAGTAAGGCC	4522
30	Imidazolinone Resistance ALS <i>Xanthium</i> spp. Ala631Asn GCT-AAT		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Ser CCG-TCG	TGATCCCG <u>A</u> ATGGTGGA	4523
		TCCACC <u>A</u> TCGGGATCA	4524
		TCCGGGTTGCTGATGCTTGCTCGATTCCGTCCACTGGTGGCG ATCACGGGGCAGGTG <u>C</u> CGCGGAATGATTGGGACGGATGCTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT	4525
		ACCGTGTACCTCAACAATAGGAGTCTCTGAAAAGCATCCGTCC CAATCATTGCCGCG <u>A</u> CACCTGCCCGTGATGCCACCAAGTGG ACGGAATCGAGCAAAGCATCAGCAAACCCGG	4526
		GGCAGGTG <u>T</u> CGCGCGA	4527
		TCGCCGCG <u>A</u> CACCTGCC	4528
	Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Gln CCG-CAG	CCGGGTTGCTGATGCTTGCTCGATTCCGTCCACTGGTGGCGA TCACGGGGCAGGTG <u>C</u> CGCGGAATGATTGGGACGGATGCTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC	4529
		GACCGTGTACCTCAACAATAGGAGTCTCTGAAAAGCATCCGTCC CCAATCATTGCCGCG <u>T</u> GCACCTGCCCGTGATGCCACCAAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG	4530
		GCAGGTG <u>C</u> AGCGCGAA	4531
		TTCGCCG <u>C</u> GCACCTGC	4532
		GACCTTACCTGCTGATGTGATTGATCTCATCAGGAGCATGTGC TGCCTATGATTCT <u>A</u> TGGTGAGCCTTAAGGATATCATTAAACGA AGGTGATGGAAGAACAGTTATTGATGTT	4533
10	Imidazolinone Resistance ALS <i>Bassia scoparia</i> Ser649Asn AGT-AAT	GAACATCAATAACTTGTCTTCATCACCTCGTTAATGATATCCTT GAAGGCTGCACCA <u>T</u> AGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	4534
		GATTCT <u>A</u> TGGTGCAG	4535
		CTGCACCA <u>T</u> AGGAATC	4536
		AGCGGGTTAGCAGACGCGATGCTTGACAGTGTCTCTTGTCGC CATTACAGGACAGGT <u>C</u> CTGCCGGATGATCGGTACTGACGCCCT CCAAGAGACACCAATCGTTGAGGTAACGAGGT	4537
		ACCTCGTTACCTCAACGATTGGTGTCTCTGGAAGGCGTCAGTAC CGATCATCCGGCGAG <u>A</u> GACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCGCT	4538
15	Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Ser CCT-TCT	GACAGGTG <u>C</u> CTGCCGG	4539
		CCGGCGAG <u>A</u> GACCTGTC	4540

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAA	GC GG GT TAG CAG ACG CG AT G CT G AC AG T GT CC CT TT GT CG CC ATTACAGGACAGGTCA <u>AC</u> CGCCGGATGATCGGTACTGACGCC CCAAGAGACACCAATCGTTGAGGTAAACGAGGT	4541
		GACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTA CCGATCATCCGGCG <u>T</u> GGACCTGTCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	4542
		ACAGGTCCA <u>AC</u> GCCGA	4543
		TCCGGCG <u>T</u> GGACCTGT	4544
10	Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAG	GC GG GT TAG CAG ACG CG AT G CT G AC AG T GT CC CT TT GT CG CC ATTACAGGACAGGT <u>CC</u> <u>AG</u> CGCCGGATGATCGGTACTGACGCC CCAAGAGACACCAATCGTTGAGGTAAACGAGGT	4545
		GACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTA CCGATCATCCGGCG <u>T</u> GGACCTGTCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	4546
		ACAGGT <u>CC</u> <u>AG</u> CGCCGA	4547
		TCCGGCG <u>C</u> GGACCTGT	4548
15	Imidazolinone Resistance ALS 1 <i>Brassica napus</i> Ser638Asn AGT-AAT	GACCATA CCT GT GG AT GT G AT AT GT CC CG ACCA AG AAC AT GT GT TACCGATGATCCC <u>A</u> GGTGGC ACT TT CAA AG AT GTA ATA AC AGA AGGGGATGGTGC <u>CA</u> TAAGTACTGAGAGAT	4549
		ATCTCTCAGTACTTAGTGC <u>G</u> ACCATCCCTTCTGTATTACATCTT TGAAAGTGC <u>C</u> ACCA <u>T</u> GGGATCATCGGTAAACACATGTTCTGGT GCGGACATATCACATCCAACAGGTATGGTC	4550
		GATCCC <u>AA</u> <u>A</u> GGTGGCA	4551
		TGCCACCA <u>T</u> GGGATC	4552
20	Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Ser CCC-TCC	CAGCGGGTTAGCAGACCGATGCTGACAGTGTCCCTTGTGCG CCATTACAGGACAGGT <u>CC</u> CTCGCCGGATGATCGGTACTGACGCC TTCCAAGAGACACCAATCGTTGAGGTAAACGAGG	4553
		CCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTACC GATCATCCGGCGAGGA <u>AC</u> CTGTCTGTAATGGCGACAAGAGGAA CACTGTCAAGCATCGCGTCTGCTAACCCGCTG	4554
		GGACAGGT <u>CC</u> CGCCG	4555
		CGGCGAGGA <u>AC</u> CTGTCC	4556
25	Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Gln CCC-CAG	AGCGGGTTAGCAGACCGATGCTGACAGTGTCCCTTGTGCG CATTACAGGACAGGT <u>CA</u> CTCGCCGGATGATCGGTACTGACGCC TCCAAGAGACACCAATCGTTGAGGTAAACGAGGT	4557
		ACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTAC CGATCATCCGGCGAG <u>G</u> ACCTGTCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4558
		GACAGGT <u>CA</u> CTCGCCG	4559

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		CCGGCGAG <u>T</u> GACCTGTC	4560
5	Imidazolinone Resistance ALS 2 <i>Brassica napus</i> Ser582Asn AGT-AAT	GACCATACTGTTGGATGTGATATGTCGGCACCAAGAACATGTGT TACCGATGAT <u>CCCAA</u> <u>A</u> TGGTGGCACTTCAAAGATGTAATAACAGA AGGGGATGGTCGCACTAAGTACTGAGAGAT	4561
		ATCTCTCAGTACTTAGTGC <u>G</u> ACC <u>C</u> ATCCCCTCTGTTATTACATCTT TGAAAGTGC <u>C</u> ACCA <u>T</u> GGGATCATCGGAACACATGTTCTGGT GCGGACATATCACATCCAACAGGTATGGTC	4562
		GAT <u>CCCAA</u> <u>A</u> TGGTGGCA	4563
		TGCCACCA <u>T</u> GGGATC	4564
10	Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGG <u>G</u> ATGCTGACAGTGT <u>C</u> CTCTCGTC <u>CC</u> CATCACAGGACAGGT <u>C</u> <u>T</u> TCGCCGGATGATCGGTACTGAC <u>CG</u> GT TCCAAGAGACGCCAATCGTTGAGGTAA <u>C</u> GGT	4565
		ACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CG</u> GT <u>C</u> AGTAC CGATCATCCGG <u>G</u> AG <u>A</u> GACCTGTC <u>T</u> GTGATGG <u>C</u> AC <u>G</u> GAGAGGA ACACTGTCAAGCATCGCG <u>T</u> GGCTAACCCGCT	4566
		GACAGGT <u>C</u> <u>T</u> TCGCCGG	4567
		CCGGCGAG <u>A</u> GACCTGTC	4568
		GC <u>GGGG</u> TTAGCCGAC <u>CG</u> GTGCTGACAGTGT <u>C</u> CTCTCGTC <u>CC</u> ATCACAGGACAGGT <u>CC</u> <u>A</u> ACGCCGGATGATCGGTACTGAC <u>CG</u> GT CCAAGAGACGCCAATCGTTGAGGTAA <u>C</u> GGT	4569
15	Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAA	GACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CG</u> GT <u>C</u> AGTA CCGATCATCCGG <u>G</u> <u>T</u> GGACCTGTC <u>T</u> GTGATGG <u>C</u> AC <u>G</u> GAGAGG AACACTGTCAAGCATCGCG <u>T</u> GGCTAACCCGCT	4570
		ACAGGT <u>CC</u> <u>A</u> ACGCCGG <u>A</u>	4571
		TCCGGCG <u>T</u> GGACCTGT	4572
		GC <u>GGGG</u> TTAGCCGAC <u>CG</u> GTGCTGACAGTGT <u>C</u> CTCTCGTC <u>CC</u> ATCACAGGACAGGT <u>CC</u> <u>A</u> CGGCCGGATGATCGGTACTGAC <u>CG</u> GT CCAAGAGACGCCAATCGTTGAGGTAA <u>C</u> GGT	4573
		GACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CG</u> GT <u>C</u> AGTA CCGATCATCCGG <u>G</u> <u>T</u> GGACCTGTC <u>T</u> GTGATGG <u>C</u> AC <u>G</u> GAGAGG AACACTGTCAAGCATCGCG <u>T</u> GGCTAACCCGCT	4574
20	Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAG	ACAGGT <u>CC</u> <u>A</u> CGGCCGG <u>A</u>	4575
		TCCGGCG <u>T</u> GGACCTGT	4576
		GC <u>GGGG</u> TTAGCCGAC <u>CG</u> GTGCTGACAGTGT <u>C</u> CTCTCGTC <u>CC</u> ATCACAGGACAGGT <u>CC</u> <u>A</u> CGGCCGGATGATCGGTACTGAC <u>CG</u> GT CCAAGAGACGCCAATCGTTGAGGTAA <u>C</u> GGT	4577
		GACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CG</u> GT <u>C</u> AGTA CCGATCATCCGG <u>G</u> <u>T</u> GGACCTGTC <u>T</u> GTGATGG <u>C</u> AC <u>G</u> GAGAGG AACACTGTCAAGCATCGCG <u>T</u> GGCTAACCCGCT	4578
		ACAGGT <u>CC</u> <u>A</u> CGGCCGG <u>A</u>	4579
25	Imidazolinone Resistance ALS 3 <i>Brassica napus</i> Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGT <u>C</u> ATCTGTC <u>CC</u> CACCAAGAACATGTGT TACCGATGAT <u>CCCAA</u> <u>A</u> TGGTGGCACTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4577
		ATCTCTCAGTACTTAGTGC <u>G</u> ACC <u>C</u> ATCCCCTCGGTATTACATCTT TGAAAGTGC <u>C</u> ACCA <u>T</u> GGGATCATCGGAACACATGTTCTGGT GCGGACAGATGACATCCAACAGGTACGGTC	4578

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		GATCCCAA <u>A</u> TGGTGGCA	4579
		TGCCACCA <u>A</u> TTGGGATC	4580
5	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCG CCATCACGGGCCAGGT <u>C</u> TC <u>CCCCGCC</u> CATGATGGCACCGACGC CTTCCAGGAGACGCCCATAGTCGAGGT <u>CACCCG</u> CT	4581
		AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAAGGCGTCGGT CCGATCATGCGGCCGGAGACCTGGCCCGT <u>GATGGC</u> GACCATCG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGGA	4582
		GCCAGGT <u>C</u> CCCCGCCGC	4583
		GCGGCGGG <u>A</u> GACCTGGC	4584
		CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGT <u>CC</u> <u>A</u> CGGCC <u>C</u> ATGATGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGT <u>CACCCG</u> CTC	4585
10	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAAGGCGTCGGT GCCGATCATGCGGCC <u>T</u> <u>GGAC</u> CTGGCCCGT <u>GATGGC</u> GACCATCG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4586
		CCAGGT <u>CC</u> <u>A</u> CGGCC <u>C</u> A	4587
		TGCGGC <u>G</u> <u>T</u> <u>GGAC</u> CTGG	4588
		CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGT <u>CC</u> <u>A</u> CGGCC <u>C</u> ATGATGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGT <u>CACCCG</u> CTC	4589
		GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAAGGCGTCGGT GCCGATCATGCGGCC <u>G</u> <u>T</u> <u>GGAC</u> CTGGCCCGT <u>GATGGC</u> GACCATC GGGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4590
15	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	CCAGGT <u>CC</u> <u>A</u> CGGCC <u>C</u> A	4591
		TGCGGC <u>G</u> <u>T</u> <u>GGAC</u> CTGG	4592
		GGCCATACTTG <u>T</u> <u>GGAT</u> ATCATCGTCCCGACCAGGAGCATGTGC TGCCTATGATCCAA <u>A</u> TGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTATCTAT	4593
		ATAGATTAATAACACAGTCTGCCATACC <u>AT</u> CCAGGATCATGTCCT TGAATGCGCCCC <u>A</u> <u>T</u> <u>GGAT</u> CATAGGCAGCACATGCTCCTGGT GCGGGACGATGATCCAACAAGTATGGCC	4594
		GATCCCAA <u>A</u> TGGGGCG CGCCCC <u>A</u> <u>T</u> <u>GGAT</u> C	4595 4596
20	Imidazolinone Resistance ALS <i>Oryza sativa</i> Ser627Asn AGT-AAT		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	CTCGCGCTCGCAGACGCGTTGCTCGACTCCGCCATGGTCGC CATCACGGGACAGGTG <u>T</u> CGCGACGCATGATTGGCACCGACGCC TTCAGGAGACGCCATCGTCGAGGTACCCGCT	4597
		AGCGGGTGACCTCGACGATGGCGTCTCTGAAAGGCGTCGGT CCAATCATGCGTCGCC <u>A</u> ACCTGTCCCGTATGGCGACCATGG GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	4598
		GACAGGTG <u>T</u> CGCGACGC	4599
		GCGTCGCC <u>A</u> ACCTGTC	4600
10	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CTCGCGCTCGCAGACGCGTTGCTCGACTCCGCCATGGTCGCC ATCACGGGACAGGTG <u>C</u> AGCGACGCATGATTGGCACCGACGCC TCAGGAGACGCCATCGTCGAGGTACCCGCTC	4601
		GAGCGGGTGACCTCGACGATGGCGTCTCTGAAAGGCGTCGGT GCCAATCATGCGTCGC <u>T</u> GCACCTGTCCCGTATGGCGACCATGG GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	4602
		ACAGGTG <u>C</u> AGCGACGCA	4603
		TGCGTCGCC <u>T</u> GCACCTGT	4604
		GGCCGTACCTCTGGATATAATCGTCCCGCACCAGGAGCATGTGT TGCCTATGATCCCTA <u>A</u> TGGTGGGGTTCAAGGATATGATCCTGG ATGGTGATGGCAGGA <u>T</u> GTGTATTGATCCGT	4605
15	Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	ACGGATCAATACACAGTCCCTGCCATCACCATCCAGGATCATATCC TTGAAAGCCCCACCA <u>T</u> AGGGATCATAGGCAACACATGCTCCTGG TGCGGGACGATTATATCCAAGAGGTACGGC	4606
		GATCCCTA <u>A</u> TGGTGGGG	4607
		CCCCACCA <u>T</u> AGGGATC	4608
		AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGT <u>C</u> TCGTCGGATGATCGGTACCGATGCTTCC CAGGAAACTCCAATTGTTGAGGTAACAAGGT	4609
		ACCTTGTTACCTCAACAATTGGAGTTCTGGAAAGCATCGGTAC CGATCATCCGACGAG <u>A</u> GA <u>T</u> GTGACCAGTGTATGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4610
20	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	GTCAAGTCTC <u>T</u> CGTCGG CCGACGAGAG <u>A</u> CTTGAC	4611 4612
		GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGT <u>C</u> ACGTCCGGATGATCGGTACCGATGCTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGT	4613
		GACCTTGTTACCTCAACAATTGGAGTTCTGGAAAGCATCGGTAC CCGATCATCCGACG <u>T</u> GGACTTGACCAGTGTATGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCACT	4614
		TCAAGT <u>C</u> CAACGTCCGG	4615
25	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		TCCGACG <u>T</u> GGACTTGA	4616
5	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAG <u>T</u> CC <u>A</u> CGCGTGGATGATCGGTACCGATGCTTCC AGGAAACTCCAATTGTTGAGGTACAAGGTC	4617
		GACCTTGTTACCTCAACAATTGGAGTTCTGGAAAGCATCGTA CCGATCATCCGACG <u>C</u> GGACTTGACCAGTATGCCACGAGAGG GATACTATCGAGCATTGATCAGCGAGACCAC	4618
		TCAAGTCC <u>A</u> CGCGTGG	4619
		TCCGACG <u>C</u> GGACTTGA	4620
10	Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	GACCTTAC <u>T</u> GTTGGATGTGATTGTC <u>CC</u> ACATCAAGAACATGTCCT GCCTATGAT <u>CCCC</u> <u>A</u> TGGAGGGGCTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4621
		TGAGGTCAATATTGTTCTCCATCAC <u>CC</u> CTGTGATCACATCTT TGAAAG <u>CCC</u> CT <u>CC</u> <u>A</u> TGGGATCATAGGCAGGACATGTTCTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4622
		GAT <u>CCCC</u> <u>A</u> TGGAGGGG	4623
		CCC <u>CC</u> <u>CC</u> <u>A</u> TGGGATC	4624
		TCTGGTCTTGCTGATGC <u>AC</u> TTGACTCAG <u>CC</u> CT <u>CC</u> CTTGTCGCC TTACTGGGCAAG <u>T</u> CC <u>CC</u> GGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGAT	4625
15	Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Ser CCC-TCC	ATCGAGTTACCTCAACAATTGGAGTCTTGAAAGCATCAGTACC AATCATACGCCGG <u>A</u> ACTTGGCCAGTAATGGCGACAAGAGGG CTGAGTCAAGAAC <u>T</u> GCATCAGCAAGACCAGA	4626
		GGCAAG <u>T</u> CC <u>CC</u> GGT	4627
		ACGCCGG <u>A</u> ACTTGCC	4628
		CTGGTCTTGCTGATGC <u>AC</u> TTGACTCAG <u>CC</u> CT <u>CC</u> CTTGTCGCCA TTACTGGGCAAG <u>T</u> CA <u>AC</u> GGCGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4629
		GATCGAGTTACCTCAACAATTGGAGTCTTGAAAGCATCAGTAC CAATCATACGCCG <u>T</u> GA <u>AC</u> TTGGCCAGTAATGGCGACAAGAGGG CTGAGTCAAGAAC <u>T</u> GCATCAGCAAGACCAG	4630
20	Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAA	GCAAG <u>T</u> CA <u>AC</u> GGCGTA	4631
		TACGCCG <u>T</u> GA <u>AC</u> TTGC	4632
		CTGGTCTTGCTGATGC <u>AC</u> TTGACTCAG <u>CC</u> CT <u>CC</u> CTTGTCGCCA TTACTGGGCAAG <u>T</u> CA <u>AC</u> GGCGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4633
		GATCGAGTTACCTCAACAATTGGAGTCTTGAAAGCATCAGTAC CAATCATACGCCG <u>T</u> GA <u>AC</u> TTGGCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAC <u>T</u> GCATCAGCAAGACCAG	4634
25	Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAG		
30	Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAG		

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Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAAGTTC <u>A</u> GC <u>G</u> CGTA	4635
	TACGCC <u>G</u> CTGA <u>A</u> TTGC	4636
Imidazolinone Resistance ALS <i>Amaranthus powellii</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA <u>A</u> CGGTGCCGCCCTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT ACCAACTAATAAGCCCTCTTCCATCACCCCTGTATGGTGTCCCT TGAAGGCGGCACC <u>G</u> TAGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATA <u>C</u> GGTC GATCCCTA <u>A</u> CGGTGCCG CGGCACCG <u>T</u> AGGGATC	4637 4638 4639 4640

Table 12
Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Porphyric Herbicide Resistant PPO <i>Arabidopsis thaliana</i> Val365Met GTT-ATG	TCTTGCGCCCTTTCTGAATCTGCTGCAAATGCACTCTCAAAACT ATATTACCCACCA <u>ATGGCAGCAGTATCTATCTCGTACCCGAAAGA</u> AGCAATCCGAACAGAATGTTGATAGATGG	4641
		CCATCTATCAAACATTCTGTTGGATTGCTTCTTCGGGTACGAGA TAGATACTGCTGCC <u>ATGGTGGGTAATATAGTTTGAGAGTCATT</u> TGCAGCAGATTAGAAAGAGGGCGCAAGA	4642
		CCCACCA <u>ATGGCAGCAG</u>	4643
		CTGCTGCC <u>ATGGTGGG</u>	4644
10	Porphyric Herbicide Resistant PPO <i>Nicotiana tabacum</i> Val376Met GTT-ATG	TATTACGTCCCTTTGGTGGCGCAGCAGATGCACTTCAAATT CTACTATCCCC <u>ATGGGAGCAGTCACAATTTCATATCCTCAAGAA</u> GCTATTCTGATGAGCGTCTGGTTGATGG	4645
		CCATCAACCAGACGCTCATCAGAATAGCTTCTGAGGATATGAA ATTGTGACTGCTCC <u>ATGGGGGATAGTAGAAATTGAAAGTGCA</u> TCTGCTGCGGCAACCGAAAGAGGGACGTAATA	4646
		TCCCC <u>CAATGGGAGCAG</u>	4647
		CTGCTCC <u>ATGGGGGA</u>	4648
		TGTTGCGTCCGCTTCGTTGGTGCAGCAGATGCATTGTCAAAT TTTATTATCCTCC <u>GATGGCAGCTGTATCAATTTCATATCCAAAAGA</u> CGCAATTCTGTGCTGACCGGCTGATTGATGG	4649
15	Porphyric Herbicide Resistant PPO <i>Cichorium intybus</i> Val383Met GTT-ATG	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTGGATATGAA ATTGATACAGCTGCC <u>ATCGGAGGATAATAAAATTGACAATGCAT</u> CTGCTGCACCAACGAAAGCGGACGCAACA	4650
		TCCTCC <u>GATGGCAGCTG</u>	4651
		CAGCTGCC <u>CATCGGAGGA</u>	4652
		TCCTTCGTCCACTTTAGATGTCGCCGAGAACATCTTTCAAATT TCATTATCCACCA <u>ATGGCAGCTGTGTCACTTCTATCCTAAAGAA</u> GCAATTAGATCAGAGTGCTTGATTGACGG	4653
		CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTAGGATAGGAA GTGACACAGCTGCC <u>ATGGTGGATAATGAAATTGAAAGAGATT</u> TGCAGGACATCTGAAAGTGGACGAAAGGA	4654
20	Porphyric Herbicide Resistant PPO <i>Spinacia oleracea</i> Val390Met GTT-ATG	TCCACCA <u>ATGGCAGCTG</u>	4655
		CAGCTGCC <u>CATGGTGGGA</u>	4656

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Porphyric Herbicide Resistant PPO <i>Zea mays</i> Val363Met GTT-ATG	TTTGCGTCCACTTCAAGCGATGCTGCAGATGCTCTATCAAGATT CTATTATCCACCGA <u>TGG</u> GCTGCTGTAAGTGTTCGATCCAAAGGAA GCAATTAGAAAAGAACGCTTAATTGATGG	4657
		CCATCAATTAAGCATTCTTCTAATTGCTTCTTGGATACGAAAC AGTTACAGCAGCC <u>A</u> CGGTGGATAATAGAACGCTTGTAGAGGACATC TGCAGCATCGCTTGAAGTGGACGAAAA	4658
		TCCACCGA <u>TGG</u> GCTGCTG	4659
		CAGCAGCC <u>A</u> CGGTGGA	4660
10	Porphyric Herbicide Resistant PPO <i>Oryza sativa</i> Val364Met GTT-ATG	TCTTGCGCCACTTCAAGTGTGAGCAGATGCTCTGTCATATT CTATTATCCACCA <u>A</u> TGGCTGCTGTAAGTGTTCATATCCAAAGAA GCAATTAGAAAAGAACGCTTAATTGACGG	4661
		CCGTCAATTAAGCATTCTTCTAATTGCTTCTTGGATATGAAAC AGTTACAGCAGCC <u>A</u> GGTGGATAATAGAACGACAGAGGACATCT GCTGCATCACTGAAAGTGGCCGCAAGA	4662
		TCCACCA <u>A</u> GGCTGCTG	4663
		CAGCAGCC <u>A</u> GGTGG	4664
		CTGGTCAAGGAGCAGGCAGCCGCCGCCGCCGAGGCCCTGGCT CCTTCGACTACCCGCC <u>A</u> GGCGCCGTGACGCTGTCGACCCG CTGAGCGCCGTGCGGGAGGAGCGCAAGGCCCTCGG	4665
15	Porphyric Herbicide Resistant PPO <i>Chlamydomonas</i> <i>reinhardtii</i> Val389Met GTG-ATG	CCGAGGCCTTGCCTCCCGCACGGCCTCAGCGGGTACGA CAGCGTCACGGGCC <u>A</u> CGCGGGTAGTCGAAGGAGGCCAGG GCCTCGGCGGGCGGCGCTGCTCCTGACCAG	4666
		ACCCGCC <u>A</u> GGCGCC	4667
		GGCGCCC <u>A</u> CGGGCGGT	4668

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Table 13
Genome-Altering Oligos Conferring Triazine Resistance

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
25	Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTACGGTTATTTGGCCGATTGAT TTCCAATATGCT <u>A</u> TTCAACAATTCTCGTTCTACATTCTCTT AGCGGCTGGCCGGTAGTAGGTATTG	4669
		CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAACGTAAGAA CGAGAATTGTTGAA <u>A</u> GTAGCATATTGAAATCAATCGGCCAAAT AACCCTGAGCAGCTACAATGTTGAAGTT	4670

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	ATATGCT <u>A</u> CTTCAACA	4671
		TGTTGAA <u>A</u> GTAGCATAT	4672
		AAACTATAACATCGTAGCCGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTCGTTACACTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4673
		CAGATACCTACTACAGGCCAACGAGCTAGGAAGAAGTGTAAAGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAAGATCAATCGGCCAAAAT TAACCATGAGCGGCTACGATTTAAGTTT	4674
		ATATGCT <u>A</u> CTTCAACA	4675
		TGTTGAA <u>A</u> GTAGCATAT	4676
	Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTATAATATCGTAGCCGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTTAACAACTCTCGCTTTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4677
		CAGATACCTACTACAGGCCAACGAGCTAGGAAGAAGAATGTAAAGAG CGAGAGTTGTTAA <u>A</u> GTAGCATATTGGAAAGATCAATCGGCCAAAAT AACCATGAGCGGCTACGATATTATAAGTTT	4678
		ATATGCT <u>A</u> CTTCAACA	4679
		TGTTAA <u>A</u> GTAGCATAT	4680
		AAACTATAATATCGTAGCCGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTCGTTACACTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4681
10	Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	CAGATACCTACTACAGGCCAACGAGCTAGGAAGAAGAATGTAAAGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAAGATCAATCGGCCAAAAT TAACCATGAGCGGCTACGATATTATAAGTTT	4682
		ATATGCT <u>A</u> CTTCAACA	4683
		TGTTGAA <u>A</u> GTAGCATAT	4684
		AAACTATAATATCGTAGCTGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTTAACAACTCTCGTCGTTACATTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4685
		CAGATACCTACTACAGGCCAACGAGCTAGGAAGAAGAATGTAAAGAA CGAGAATTGTTGAA <u>A</u> GTAGCATATTGGAAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACGATATTATAAGTTT	4686
15	Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	ATATGCT <u>A</u> CTTCAACA	4687
		TGTTGAA <u>A</u> GTAGCATAT	4688
		AAACCTATAATATTGAGCAGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCT <u>A</u> CTTCAACAACTCTCGTCGTTACATTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4689
		CAGATACCTACTACAGGCCAACGAGCTAGGAAGAAGAATGTAAAGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAAGATCAATCGGCCAAAAT TAACCATGAGCTGCTACAATTATAAGTTT	4690
		ATATGCT <u>A</u> CTTCAACA	4691
20	Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT		
25	Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	TGTTGAAAGTAGCATAT	4692
		AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTCACAATTCTCGTTCTTACATTCTTCT TAGCTGCTGGCCTGTAGTAGGTATTG	4693
		CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAGGTT	4694
		ATATGCAAC T TTCAACA	4695
		TGTTGAAAGTAGCATAT	4696
10	Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCT A TTCAACAATTCTCGTTCTTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTG	4697
		CAAATACCTACTACCCGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGAAGTT	4698
		ATATGCT A TTCAACA	4699
		TGTTGAAAGTAGCATAT	4700
		AAACTTATAATATTGTGGCCGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTACTTTAACAACTCTCGTTCTTACACTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTG	4701
15	Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	CAAATCCCTACTACAGGCCAAGCAGCCAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTT	4702
		ATATGCT A TTTAACA	4703
		TGTTAAAAGTAGCATAT	4704
		AGACTTATAATATTGTGGCTGCTCACGGTTATTTGGTCGATTAAT CTTCCAATATGCTACTTTAACAAATTCTCGTTCTTACACTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4705
		CAGATCCCTACTACAGGCCAAGCAGCCAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCCAAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	4706
20	Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	ATATGCT A TTCAACA	4707
		TGTTGAAAGTAGCATAT	4708
		AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT TTTCCAATATGCT A TTCAACAATTCTCGTTCTTACATTCTTCT AGCGGCTTGGCCGGTAGTAGGTATTG	4709
		CAAATACCTACTACCCGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCCAAAAT AACCGTGAGCAGCTACAATGTTGAAGTT	4710
		ATATGCT A TTCAACA	4711
25	Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	TGTTGAAAGTAGCATAT	4712

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGCCGATTGAT CTTCCAATATGCT <u>A</u> TTCAACA <u>C</u> TCGTT <u>G</u> TACACTTCC TAGCTGCTGGCCTGTAGTAGGTATCTG	4713
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAA <u>C</u> GAA CGAGAGTTGTT <u>G</u> AA <u>A</u> GTAGCATATT <u>G</u> GAAGATCAATCGGCCAAA TAACC <u>A</u> TGAGCGGCTACGAT <u>T</u> ATAAGTT	4714
		ATATGCT <u>A</u> CTTCAACA	4715
		TGTTGAA <u>A</u> GTAGCATAT	4716
10	Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGCCGATTGAT CTTCCAATATGCT <u>A</u> CTTCAACA <u>C</u> TCGCT <u>G</u> TACATTCTTCT TAGCTGCTGGCCTGTAGTAGGTATCTG	4717
		CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAA <u>A</u> GTAA <u>A</u> GAG CGAGAGTTGTT <u>G</u> AA <u>A</u> GTAGCATATT <u>G</u> GAAGATCAATCGGCCAAA AACCATGAGCGGCTACGATATTATAAGTT	4718
		ATATGCT <u>A</u> CTTCAACA	4719
		TGTTAAA <u>A</u> GTAGCATAT	4720
		AAACTTATAATATCGTAGCCGCTCATGGTTATTTGCCGATTGAT CTTCCAATATGCT <u>A</u> CTTCAACA <u>C</u> TCGTT <u>G</u> TACACTTCC TAGCTGCTGGCCTGTAGTAGGTATCTG	4721
15	Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAA <u>C</u> GAA CGAGAGTTGTT <u>G</u> AA <u>A</u> GTAGCATATT <u>G</u> GAAGATCAATCGGCCAAA TAACC <u>A</u> TGAGCGGCTACGATATTATAAGTT	4722
		ATATGCT <u>A</u> CTTCAACA	4723
		TGTTGAA <u>A</u> GTAGCATAT	4724
		AAACTTATAATATCGTAGCT <u>G</u> CTCATGGTTATTTGCCGATTGAT CTTCCAATATGCT <u>A</u> CTTCAACA <u>C</u> ATT <u>G</u> TCGTT <u>G</u> TACATTCTTCC TAGCTGCTGGCCTGTAGTAGGTATCTG	4725
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAA <u>A</u> GTAA <u>A</u> GAA CGAGAATTGTT <u>G</u> AA <u>A</u> GTAGCATATT <u>G</u> GAAGATCAATCGGCCAAA AACCATGAGCAGCTACGATATTATAAGTT	4726
20	Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	ATATGCT <u>A</u> CTTCAACA	4727
		TGTTGAA <u>A</u> GTAGCATAT	4728
		AAACCTTATAATATTGAGCTCATGGTTATTTGCCGATTGAT CTTCCAATATGCT <u>A</u> CTTCAACA <u>C</u> ACTCTCGTT <u>G</u> TACATTCTTCC TAGCTGCTGGCCTGTAGTAGGTATCTG	4729
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAA <u>A</u> GTAA <u>A</u> GAA CGAGAGTTGTT <u>G</u> AA <u>A</u> GTAGCATATT <u>G</u> GAAGATCAATCGGCCAAA TAACC <u>A</u> TGAGCT <u>G</u> CTACAATTATAAGTT	4730
		ATATGCT <u>A</u> CTTCAACA	4731
25	Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT	TGTTGAA <u>A</u> GTAGCATAT	4732

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTCAACAATTCTCGTTCTTACATTCTCT TAGCTGCTTGGCCTGTAGTAGGTATTG	4733
		CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACAATATTAGGTT	4734
		ATATGCAACTTCAACA	4735
		TGTTGAAAGTAGCATAT	4736
		AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAATTCTCGTTCTTACATTCTCT TAGCGGCTTGGCCGGTAGTAGGTATTG	4737
10	Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	CAAATACCTACTACCCGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTT	4738
		ATATGCTACTTCAACA	4739
		TGTTGAAAGTAGCATAT	4740
		AAACTTATAATATTGTGGCCGCTCATGGTTATTTGGCCGATTAAAT CTTCCAATATGCTACTTCAACAATTCTCGTTCTTACACTCTCT TGGCTGCTTGGCCTGTAGTAGGGATTG	4741
		CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTT	4742
15	Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	ATATGCTACTTCAACA	4743
		TGTTAAAAGTAGCATAT	4744
		AGACTTATAATATTGTGGCTGCTCACGGTTATTTGGTCGATTAAAT CTTCCAATATGCTACTTCAACAATTCTCGTTCTTACACTCTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4745
		CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCAAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	4746
		ATATGCTACTTCAACA	4747
20	Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	TGTTGAAAGTAGCATAT	4748
		AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT TTTCCAATATGCTACTTCAACAATTCTCGTTCTTACATTCTCT AGCGGCTTGGCCGGTAGTAGGTATTG	4749
		CAAATACCTACTACCCGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTT	4750
		ATATGCTACTTCAACA	4751
		TGTTGAAAGTAGCATAT	4752
25	Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Triazine Resistant D1 Protein <i>Picea abies</i> Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTCGGCCGATTGAT CTTCCAGTATGCTACTTCAACAACCTCCCGTTCTTACATTCTTCT TAGCTGCTTGGCCCGTAGCAGGTATCTG	4753
	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGGGAGTTGTTGAAAGTAGCATACTGGAAAGATCAATCGGCCAAA TAACCGTGAGCAGCCACAATATTGTAGGTT	4754
	GTATGCTACTTCAACA	4755
	TGTTGAAAGTAGCATA	4756
10 Triazine Resistant D1 Protein <i>Vicia faba</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTCGGCCGATTGAT CTTCCAATATGCTACTTCAACAATTCTCGCTCTTACATTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4757
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAAGATCAATCGGCCAAAAT AACCCTGAGCAGCTACAATATTAGGTT	4758
	ATATGCTACTTCAACA	4759
	TGTTGAAAGTAGCATA	4760
	AGACTTATAATATTGTGGCTGCTCATGGTTATTCGGCCGATTAAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCTTACACTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4761
15 Triazine Resistant D1 Protein <i>Hordeum vulgare</i> Ser264Thr AGT-ACT	CAGATTCTACTACAGGCCAAGCAGCCAAGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAAGATTAATCGGCCAAAAT AACCCTGAGCAGCCACAATATTATAAGTCT	4762
	ATATGCTACTTCAACA	4763
	TGTTGAAAGTAGCATA	4764
	AAACTTATAATATTGTGGCTGCTCATGGTTATTCGGCCGATTAAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCTTACACTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4765
20 Triazine Resistant D1 Protein <i>Triticum aestivum</i> Ser264Thr AGT-ACT	CAGATTCTACTACAGGCCAAGCAGCCAAGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAAGATTAATCGGCCAAAAT AACCCTGAGCAGCCACAATATTATAAGTCT	4766
	ATATGCTACTTCAACA	4767
	TGTTGAAAGTAGCATA	4768
	AAACTTATAATATTGTAGCTGCTCATGGTTATTCGGCCGATTAATC TTCCAATATGCAACTTCAACAATTCTCGTTCTTACATTCTTCT AGCTGCTTGGCCTGTAGTAGGTATTG	4769
	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAAGATTAATCGGCCAAAAT AACCCTGAGCAGCTACAATATTATAAGTCT	4770
25 Triazine Resistant D1 Protein <i>Vigna unguiculata</i> Ser264Thr AGT-ACT	ATATGCAACTTCAACA	4771
	TGTTGAAAGTAGCATA	4772

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Triazine Resistant D1 Protein <i>Lotus japonicus</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTCAACAACCTCTCGTTCTTACACTTCTCT TAGCTGCTGGCCTGTTAGGTATCTG	4773
		CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACC GTGAGCAGCTACAATATTAGGTTT	4774
		ATATGCAAC <u>TTT</u> CAACA	4775
		TGTTGAAAGTAGCATAT	4776
10	Triazine Resistant D1 Protein <i>Sinapis alba</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAATTCTCGTTCTTACATTCTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4777
		CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACC GTGAGCAGCTACAATGTTGAAGTT	4778
		ATATGCT <u>ACTT</u> CAACA	4779
		TGTTGAAAGTAGCATAT	4780
15	Triazine Resistant D1 Protein <i>Pisum sativum</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAATTCTCGCTCTTACATTCTCC TAGCTGCTGGCCTGTTAGTAGGTATCTG	4781
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACC GTGAGCAGCTACAATATTAGGTTT	4782
		ATATGCT <u>ACTT</u> CAACA	4783
		TGTTGAAAGTAGCATAT	4784
20	Triazine Resistant D1 Protein <i>Spinacia oleracea</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGTCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCTTACACTTCTCT TAGCTGCTGGCCTGTTAGTAGGTATTTG	4785
		CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGACCAAAAT AACC ATGAGCAGCTACGATATTATAAGTTT	4786
		ATATGCT <u>ACTT</u> CAACA	4787
		TGTTGAAAGTAGCATAT	4788
25	Triazine Resistant D1 Protein <i>Nicotiana debneyi</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCTTACACTTCTCC TAGCTGCTGGCCTGTTAGTAGGTATCTG	4789
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACC ATGAGCAGCTACGATGTTATAAGTTT	4790
		ATATGCT <u>ACTT</u> CAACA	4791
		TGTTGAAAGTAGCATAT	4792

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Triazine Resistant D1 Protein <i>Solanum nigrum</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGCCGATTGAT CTTCCAATATGCTACTTCAACAACCTCGTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4793
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTT	4794
		ATATGCTACTTCAACA	4795
		TGTTGAAAGTAGCATAT	4796
10	Triazine Resistant D1 Protein <i>Nicotiana</i> <i>plumbaginifolia</i> Ser264Thr AGT-ACT	AAACTTATAAACATCGTAGCCGCTCATGGTTATTTGCCGATTGAT CTTCCAATATGCTACTTCAACAACCTCGTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4797
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTT	4798
		ATATGCTACTTCAACA	4799
		TGTTGAAAGTAGCATAT	4800

Example 6
Engineering male- or female-sterile plants

Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, 5 for example, AGAMOUS (AG), APETALA1 (AP1), and APETALA3 (AP3) and PISTILLATA (PI) in *Arabidopsis thaliana*, and DEFICIENS A (DEFA), GLOBOSEA (GLO), SQUAMOSA (SQUA), and PLENA (PLE) in *Antirrhinum majus*. Genetic studies have shown that the DEFA, GLO and AP3 genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box 10 genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

Altering the expression of these genes results in altered floral morphology. For example, mutations in AP3 and PI result in male-sterile flowers because petals develop in place of stamens.

15 The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

Table 14
Oligonucleotides to produce male-sterile plants

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
20	Male-sterile AP3 <i>Arabidopsis thaliana</i> Arg3Term AGA-TGA	TTGTCCTCTCCACCAAATCTCTCAACAAAAAGATTAAACAAAGAGA GAAGAACATGGCGTGAGGGAGATCCAGATCAAGAGGTAGAGAA CCAGACAAACAGACAAGTGACGTATTCAA	4801
		TTGAATACGTCACTTGTCTGTTGTTCTATCCTCTTGATC TGGATCTTCCCTCACGCCATATTCTCTCTTTGTTAACCTTTT GTTGAAGAGAGATTGGTGGAGAGGACAA	4802
		ATATGGCGTGAGGGAG	4803
		CTTCCCTCACGCCATAT	4804
		TCTCCACCAAATCTCTCAACAAAAAGATTAAACAAAGAGAGAAGA ATATGGCGAGAGGGTAGATCCAGATCAAGAGGTAGAGAACCCAGA CAAACAGACAAGTGACGTATTCAAAGAGAA	4805
25	Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys5Term AAG-TAG	TTCTCTTGAATACGTCACTTGTCTGTTGTTCTATCCTC TTGATCTGGATCTACCCCTCTGCCATATTCTCTCTTTGTTAAC CTTTTGTGAAGAGATTGGTGGAGA	4806
		CGAGAGGGTAGATCCAG	4807

	CTGGATCT <u>ACCCCTCTCG</u>	4808	
5	Male-sterile AP3 <i>Arabidopsis thaliana</i> Gln7Term CAG-TAG	CCAATCTCTCAACAAAAAGATTAAACAAGAGAGAAGAATATGG CGAGAGGGAGAT <u>CTAGATCAAGAGGATAGAGAACCGACAAACA</u> GACAAGTGA <u>CGTATTCAAAGAGAAGGAATG</u>	4809
		CATTCC <u>TTCTTGAATACGTCACTTGTCGTTGTCTGGTTCTCT</u> ATCCTCTTGAT <u>CTAGATCTCCCTCGCCATATTCTCTCTTTG</u> TTAATCT <u>TTTGTGAAGAGATTGG</u>	4810
		GGAAGAT <u>CTAGATCAAG</u>	4811
		CTTGAT <u>CTAGATCTCC</u>	4812
		CTCTCAACAAAAAGATTAAACAAGAGAGAAGAATATGGCGAGAG GGAAGAT <u>CCAGATCTAGAGGATAGAGAACCGACAAACAGACAAG</u> TGACGTATT <u>CAAAGAGAAGGAATGGTTAT</u>	4813
10	Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys9Term AAG-TAG	ATAACCATT <u>CCCTCTCTTGAATACGTCACTTGTCGTTGTCTGG</u> TTCTCTAT <u>CCCTCTAGATCTGGATCTCCCTCGCCATATTCTCTC</u> TCTTGT <u>TTAATCTTTGTGAAGAG</u>	4814
		TCCAGAT <u>CTAGAGGATA</u>	4815
		TATCCT <u>CTAGATCTGA</u>	4816
		AGAGGGAA <u>AGATCCAGATCAAGAGGATAGAGAACCGACCAACCGA</u> CAAGTGACGTATT <u>CTTAGAGAAGAAATGGTTGTCAAGAAAGCTC</u> ACGAGCTTACAG <u>TTTATGTGATGCTAGGG</u>	4817
		CCCTAGCATCACATAAA <u>ACTGTAAGCTCGTGAGCCTTCTGAACAA</u> ACCATT <u>TTCTCTCTAGAATACGTCACTTGTCGGTTGGTCTGGTC</u> TCTATCCT <u>CTTGATCTGGATCTCCCTCT</u>	4818
15	Male-sterile AP3 <i>Brassica oleracea</i> Lys23Term AAG-TAG	CGTATT <u>CTTAGAGAAGA</u>	4819
		TCTTCT <u>CTAAGAATACG</u>	4820
		GGGAAGAT <u>CCAGATCAAGAGGATAGAGAACCGACCAACCGACAA</u> GTGACGTATT <u>CTAAGTGAAGAAATGGTTGTCAAGAAAGCTCACG</u> AGCTTACAG <u>TTTATGTGATGCTAGGGTT</u>	4821
		AAACCCTAGCATCACATAAA <u>ACTGTAAGCTCGTGAGCCTTCTGAA</u> CAAACCATT <u>CTTCACTAGAATACGTCACTTGTCGGTTGGTCTGG</u> TTCTCTAT <u>CCCTCTTGATCTGGATCTCCC</u>	4822
		ATT <u>CTAAGTGAAGAAAT</u>	4823
20	Male-sterile AP3 <i>Brassica oleracea</i> Arg24Term AGA-TGA	ATT <u>TTCTCACTTAGAAT</u>	4824
		AAGATCC <u>AGATCAAGAGGATAGAGAACCGACCAACCGACAAAGTG</u> ACGTATT <u>CTAAGAGATGAATGGTTGTCAAGAAAGCTCACGAGC</u> TTACAG <u>TTTATGTGATGCTAGGGTTCGA</u>	4825
		TCGAAAC <u>CCCTAGCATCACATAAAACTGTAAGCTCGTGAGCCTTCTT</u> GAACAA <u>ACCACTTCATCTCTAGAATACGTCACTTGTCGGTTGGTC</u> TGGT <u>CTCTATCCCTTGATCTGGATCTT</u>	4826
		CTAAGAGA <u>TGAATGGT</u>	4827
		ACCATT <u>TCATCTCTTAG</u>	4828

5	Male-sterile AP3 <i>Brassica oleracea</i> Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCGACCAACCAGACAAGTGACGTATTCTA AGAGAAGAAATGGTAGTTCAAGAAAGCTCACGAGCTTACAGTTT ATGTGATGCTAGGGTTCGATTATCATGTT	4829
		AACATGATAATCGAACCCCTAGCATCACATAAAACTGTAAGCTCGT GAGCTTCCTGAAC <u>T</u> AAACCATTCTCTCTAGAATACGTCACTTGT CGGTTGGTCTGGTTCTATCCTCTGA	4830
		AAATGGTT <u>A</u> GGTCAAGA	4831
		TCTTGAAC <u>T</u> AAACCATT	4832
		GGCTCGAGGGAAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGCAGGTCACCT <u>A</u> G <u>T</u> CCAAGAGAACGAAATGGTTGTTCAAGAA AGCACACGAGCTCTGTTCTGTGATGCT	4833
10	Male-sterile AP3 <i>Brassica napus</i> Tyr21Term TAC-TAG	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTGAACAAACC ATTTCCTCTGG <u>A</u> CTAGGTGACCTGCCTGTTGTTGGTTCTA TCCTCTTAATCTGGATCTTCCCTCGAGCC	4834
		GTCACCT <u>A</u> G <u>T</u> CCAAGAG	4835
		CTCTTGG <u>A</u> CTAGGTGAC	4836
		CGAGGGAAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGG CAGGTCACCTACTCCT <u>A</u> GAGAACGAAATGGTTGTTCAAGAAAGCAC ACGAGCTCTGTTCTGTGATGCTAAAG	4837
15	Male-sterile AP3 <i>Brassica napus</i> Lys23Term AAG-TAG	CTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTGAACAA ACCATTCTCT <u>A</u> GGAGTAGGTGACCTGCCTGTTGTTGGTT TCTATCCTCTTAATCTGGATCTTCCCTCG	4838
		CCTACTCCT <u>A</u> GAGAACGAA	4839
		TCTTCTCT <u>A</u> GGAGTAGG	4840
		GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAG <u>T</u> GAAGAACGAAATGGTTGTTCAAGAAAGCACACG AGCTCTCTGTTCTGTGATGCTAAAGTTT	4841
20	Male-sterile AP3 <i>Brassica napus</i> Arg24Term AGA-TGA	AAACTT <u>A</u> GCATCACAGAGAACAGAGAGCTCGTGTGCTTCTGA CAAACCAATTCT <u>C</u> ACTGGAGTAGGTGACCTGCCTGTTGTTGG TTCTCTATCCTCTTAATCTGGATCTTCCC	4842
		ACTCCAAG <u>T</u> GAAGAAC	4843
		ATTCTC <u>A</u> CTTGGAGT	4844
		AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTC ACCTACTCCAAGAGAT <u>G</u> AAATGGTTGTTCAAGAAAGCACACGAGC TCTCTGTTCTGTGATGCTAAAGTTCCA	4845
25	Male-sterile AP3 <i>Brassica napus</i> Arg25Term AGA-TGA	TGGAAACTT <u>A</u> GCATCACAGAGAACAGAGAGCTCGTGTGCTTCTT GAACAAACCAATT <u>C</u> ACTCTTGGAGTAGGTGACCTGCCTGTTGTT TGGTTCTCTATCCTCTTAATCTGGATCTT	4846
		CCAAGAG <u>A</u> GAATGGT	4847
		ACCATT <u>C</u> ATCTCTTGG	4848

	Male-sterile DEFA <i>Antirrhinum majus</i> Arg3Term CGA-TGA	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGT AGTGGTCGATGGCTGAGGGAAAGATCCAGATTAAGAGGATAGAG AACCAAACAAACAGGCAGGTACCTACTCCA TGGAGTAGGTGACCTGCCTGTTGGTTCTATCCTCTTAAT CTGGATCTCCCTCAAGCCATCGAACCACTACCACTACTGCTCTG TTTCTTCTCCAGCTTCCTTCTCTCC CGATGGCTGAGGGAAAG CTTCCCTCAAGCCATCG	4849 4850 4851 4852
5	Male-sterile DEFA <i>Antirrhinum majus</i> Lys5Term AAG-TAG	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGGTAGATCCAGATTAAGAGGATAGAGAACCAA ACAAACAGGCAGGTACCTACTCCAAGAGAA TTCTCTGGAGTAGGTGACCTGCCTGTTGGTTCTATCCT CTTAATCTGGATCTACCCCTCGAGCCATCGAACCACTACCAACTG CTCTTGTTCTTCTCCAGCTTCCTT CTCGAGGGTAGATCCAG CTGGATCTACCCCTCGAG	4853 4854 4855 4856
10	Male-sterile DEFA <i>Antirrhinum majus</i> Gln7Term CAG-TAG	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTCGATG GCTCGAGGGAAAGATCTAGATTAAGAGGATAGAGAACCAAACAAAC AGGCAGGTACCTACTCCAAGAGAAATG CATTTCTCTGGAGTAGGTGACCTGCCTGTTGGTTCTC TATCCTCTTAATCTAGATCTCCCTCGAGCCATCGAACCACTACCA CTACTGCTCTGTTCTTCTCCAGCTT GGAAGATCTAGATTAAG CTTAATCTAGATCTCC	4857 4858 4859 4860
15	Male-sterile DEFA <i>Antirrhinum majus</i> Lys9Term AAG-TAG	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTCGATGGCTCGA GGGAAGATCCAGATTAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGAGAAGAAATGGTTGT ACAAACCATTTCTCTGGAGTAGGTGACCTGCCTGTTGGTT GTTCTCTATCCTCTAAATCTGGATCTCCCTCGAGCCATCGAACCA CTACCACTACTGCTCTGTTCTTCTTC TCCAGATTAGAGGATA TATCCTCTAAATCTGGA	4861 4862 4863 4864
20	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys5Term AAG-TAG	TCACTTAAAGATCTCAAACCTTGAGCAAAAGAAAAAAAC TATGGCTCGTGGTAGATCCAGATCAAGAGAATAGAGAACCAAAC AAACAGACAAGTCACCTATTCTAAGAGAA TTCTCTAGAATAAGTAGTGACTTGCTGTTGGTTCTCTATTCTC TTGATCTGGATCTACCCACGAGCCATAGTTTTTTCTTTTGCTC AAAGTTGAGATCTAAGAATTACTGA CTCGTGGTAGATCCAG CTGGATCTACCCACGAG	4865 4866 4867 4868
25			

5	Male-sterile AP3 <i>Nicotiana tabacum</i> Gln7Term CAG-TAG	ATTCTTAAGATCTCAAACITTGAGCAAAAGAAAAAAACTATGGC TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAACAAACAGA CAAGTCACCTATTCTAAGAGAAGAAATG	4869
		CATTTCTCTCTAGAATAAGTGA CTTGACTGTCTGTTGGT TCTCT ATTCTCTGATCTAGATCTCCCACGAGCCATAGTTTTTTCTTT	4870
		TTGCTCAAAGTTGAGATCTAAGAAT GGAAGATCTAGATCAAG	4871
		CTTGTATCTAGATCTCC	4872
		AAGATCTCAAACITTGAGCAAAAGAAAAAAACTATGGCTCGTG GGAAGATCCAGATCTAGAGAATAGAGAACCAACAAACAGACAAGT CACTTATTCTAAGAGAAGAAATGGACTTT	4873
10	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys9Term AAG-TAG	AAAGTCCATTTCTCTCTAGAATAAGTGA CTTGACTGTCTGTTGG TTCTCTATTCTCTAGATCTGGATCTCCCACGAGCCATAGTTTTTT	4874
		TTCTTTTGCTCAAAGTTGAGATCTT TCCAGATCTAGAGAATA	4875
		TATTCTCTAGATCTGGA	4876
		ATCTCAAACITTGAGCAAAAGAAAAAAACTATGGCTCGGG AGATCCAGATCAAGTGA ATAGAGAAGAACCAACAAACAGACAAGTCAC TTATTCTAAGAGAAGAAATGGACTTTCA	4877
		TGAAAAGTCCATTTCTCTCTAGAATAAGTGA CTTGACTGTCTGTTGG TGGTTCTCTATTCA CTGATCTGGATCTCCCACGAGCCATAGTT TTTTTCTTTGCTCAAAGTTGAGAT	4878
15	Male-sterile AP3 <i>Nicotiana tabacum</i> Arg10Term AGA-TGA	AGATCAAGTGAATAGAG	4879
		CTCTATTCACTTGATCT	4880
		GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAAACGAA CAGACAAGTAAC TAGTCAAACGAGGGATGGTCTTCAAGAAG GCCAATGAGCTCACTGTTCTTGATGCT	4881
		AGCATCACAAAGAACAGTGA GCTATTGGCCTTCTGAAAAGACCA TCCCTTCGTTTGACTAAGTTACTGTCTGTTGTTCTAT TCTCTTGATCTGGATCTTCCTCGAGCC	4882
		GTAAC TTAGTCAAACG	4883
20	Male-sterile AP3 <i>Medicago sativa</i> Tyr21Term TAC-TAG	CGTTTGACTAAGTTAC	4884
		GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAAACGAA CAGACAAGTAAC TACTGAAAACGAGGGATGGTCTTCAAGAAG GCCAATGAGCTCACTGTTCTTGATGCT	4881
		AGCATCACAAAGAACAGTGA GCTATTGGCCTTCTGAAAAGACCA TCCCTTCGTTTGACTAAGTTACTGTCTGTTGTTCTAT TCTCTTGATCTGGATCTTCCTCGAGCC	4882
		GTAAC TTAGTCAAACG	4883
		CGTTTGACTAAGTTAC	4884
25	Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA	CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAAACGAA GACAAGTAAC TACTGAAAACGAGGGATGGTCTTCAAGAAG CAATGAGCTCACTGTTCTTGATGCTAA	4885
		TTAGCATCACAAAGAACAGTGA GCTATTGGCCTTCTGAAAAGAC CATCCCTTCGTTTGACTAAGTTACTGTCTGTTGTTCT ATTCTCTTGATCTGGATCTTCCTCGAG	4886
		AACTTACTGAAAACGAA	4887
		TTCGTTTGACTAAGTT	4888

5	Male-sterile AP3 <i>Medicago sativa</i> Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACCTACTCATACGAAGGGATGGCTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTGTGATGCTAAGG	4889
		CCTTAGCATCACAAAGAACAGTGAGCTATTGGCCTTCTGAAAAG ACCATCCCTCGTTATGAGTAAGTTACTTGTCTGTTGTGTTCT	4890
		CTATTCTCTGATCTGGATCTTCCTCG	
		CTTACTCATACGAAGG	4891
		CCTTCGTTATGAGTAAG	4892
10	Male-sterile AP3 <i>Medicago sativa</i> Arg24Term CGA-TGA	GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACCTACTCAAATGAAGGGATGGCTTTCAAGAAGGCCAATG AGCTCACTGTTCTTGTGATGCTAAGGTT	4893
		AAACCTTAGCATCACAAAGAACAGTGAGCTATTGGCCTTCTGAA AAGACCATCCCTCATTTGAGTAAGTTACTTGTCTGTTGTGTT	4894
		TCTCTATTCTCTGATCTGGATCTTC	
		ACTCAAATGAAGGGAT	4895
		ATCCCTTCATTTGAGT	4896
15	Male-sterile DEF4 <i>Solanum tuberosum</i> Tyr21Term TAT-TAG	GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTAGTCAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACCTACAGTTCTTGTGATGCT	4897
		AGCATCACAAAGAACTGTAAGTTCAATTAGCCTTCTGAATAGCCC TTTCTCTCTTGAAGTCACCTGCCTATTGTTGGTTTCTATT	4898
		TTCTTGATCTGGATCTTACCAACGAGCC	
		GTGACTTAGTCAAAGAG	4899
		CTCTTGAAGTCAC	4900
20	Male-sterile DEF4 <i>Solanum tuberosum</i> Ser22Term TCA-TGA	CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATTGAAAGAGAAGAAATGGGCTATTCAAGAAGGCT AATGAACCTACAGTTCTTGTGATGCTAA	4901
		TTAGCATCACAAAGAACTGTAAGTTCAATTAGCCTTCTGAATAGCC CATTCTCTCTTGAATAAGTCACCTGCCTATTGTTGGTTTCTA	4902
		TTTCTTGATCTGGATCTTACCAACGAG	
		GACTTATTGAAAGAGAA	4903
		TTCTCTTCAATAAGTC	4904
25	Male-sterile DEF4 <i>Solanum tuberosum</i> Lys23Term AAG-TAG	CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGC AAGTGACTTATTCAAGAGAAGAAATGGGCTATTCAAGAAGGCTAA TGAACCTACAGTTCTTGTGATGCTAAAG	4905
		CTTAGCATCACAAAGAACAGTGAGTTCAATTAGCCTTCTGAATAGC CCATTCTCTCTATGAATAAGTCACCTGCCTATTGTTGGTTTCT	4906
		TATTGTTGATCTGGATCTTACCAACG	
		CTTATTCAAGAGAAGA	4907
		TCTCTCTATGAATAAG	4908

5	Male-sterile DEF4 <i>Solanum tuberosum</i> Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAAG TGACTTATTCAAAGTGAAGAAAATGGGCATTCAAGAAGGCTAAATGA ACTTACAGITCTTGTGATGCTAAAGTTT	4909
		AAACTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAAT AGCCCATTCTTC <u>ACTT</u> GAATAAGTCACTTGCCTATTGTTGGTT TTCTATTCTTGATCTGGATCTTACC	4910
		ATTCAAAG <u>T</u> GAAGAAAT	4911
		ATTTC <u>TTCA</u> TTGAAT	4912
		GCTAATGAACTTACTGTTCTTGTGATGCTAAAGTTCAATTGTTAT GATTCTAGTACT <u>T</u> GAAGAACTTCATGAGTTATAAGTCCCTATCA CGACCAAAACAATTGTTCGATCTGTACC	4913
10	Male-sterile AP3 <i>Lycopersicon esculentum</i> Gly27Term GGA-TGA	GGTACAGATCGAACATTGTTGGTCGTGATAGAGGGACTTATAAA CTCATGAAGTTTC <u>CAAG</u> TACTAGAAATCATAACAATTGAAACTTAG CATCACAAAGAACAGTAAGTTCATTAGC	4914
		CTAGTACT <u>T</u> GAAGAACTT	4915
		AAGTTTC <u>CAAG</u> TACTAG	4916
		AATGAACTTACTGTTCTTGTGATGCTAAAGTTCAATTGTTATGAT TTCTAGTACTGG <u>A</u> ACTTCATGAGTTATAAGTCCCTATCACGA CCAAACAATTGTTCGATCTGTACCAGA	4917
15	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys28Term AAA-TAA	TCTGGTACAGATCGAACATTGTTGGTCGTGATAGAGGGACTTAT AAACTCATGAAGTT <u>ATCC</u> AGTACTAGAAATCATAACAATTGAAACTT TAGCATCACAAAGAACAGTAAGTTCATT	4918
		GTACTGG <u>A</u> ACTTCAT	4919
		ATGAAGTT <u>ATCC</u> CAGTAC	4920
		ACTGTTCTTGTGATGCTAAAGTTCAATTGTTATGATTCTAGTAC TGGAAAACCTCAT <u>T</u> AGTTATAAGTCCCTATCACGACCAAACAAT TGTTCGATCTGTACCAGAACAGTATTG	4921
20	Male-sterile AP3 <i>Lycopersicon esculentum</i> Glu31Term GAG-TAG	CAATAGTCTTCTGGTACAGATCGAACATTGTTGGTCGTGATAGA GGGACTTATAAA <u>CTAAT</u> GAAGTTCCAGTACTAGAAATCATAACAA TTGAAACTTTAGCATCACAAAGAACAGT	4922
		AACTTCAT <u>T</u> AGTTATA	4923
		TATAAA <u>CTAAT</u> GAAGTT	4924
		ATTGTTATGATTCTAGTACTGGAAAACCTCATGAGTTATAAGTCC CTCTATCACGAC <u>CTAACAA</u> TTGTTCGATCTGTACCAGAACAGTATT GGAGTTGATTTGGACTACTCACTATG	4925
		CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTCTGGTACAG ATCGAACAA <u>TTGTTAGGT</u> CGTGTAGAGGGACTTAAACTCATGA AGTTTCCAGTACTAGAAATCATAACAA	4926
25	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys40Term AAA-TAA	TCACGAC <u>CTAACAA</u> TTG	4927
		CAATTGTT <u>AGGT</u> CGTGA	4928

5	Male-sterile AP3 <i>Triticum aestivum</i> Tyr21Term TAC-TAG	GGGGCGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCT <u>AGTCCAAGCGCCGGTCGGGATCATGAAG</u> AAGGCAGGGAGCTACCGTCTGCGACGCC	4929
		GGCGTCGCAGAGCACGGTGAGCTCCCGCCTTCTCATGATCC CCGACCGGGCCTGGACTAGGTACACCTGCCCTGGTGGCGTTC TCGATCCGTTTATCTCAATCTCCCCGCC	4930
		GTGACCT <u>AGTCCAAGCG</u>	4931
		CGCTTGGACTAGGTAC	4932
10	Male-sterile AP3 <i>Triticum aestivum</i> Lys23Term AAG-TAG	GGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGACCTACTCCT <u>AGCGCCGGTCGGGATCATGAAGAAGG</u> CCGCGGAGCTACCGTCTGCGACGCCAGG	4933
		CCTGGCGTCGCAGAGCACGGTGAGCTCCCGCCTTCTCATG ATCCCCGACC GGCGCT <u>AGGAGTAGGTACACCTGCCCTGGTGGC</u> GTTCTCGATCCGTTTATCTCAATCTCCCCCG	4934
		CCTACTCCT <u>AGCGCCGG</u>	4935
		CCGGCGCT <u>AGGAGTAGG</u>	4936
15	Male-sterile AP3 <i>Triticum aestivum</i> Ser26Term TCG-TAG	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACTCCAAGCGCCGGT <u>AGGGGATCATGAAGAAGGCGCGGAGCTC</u> ACCGTGCTCTGCGACGCCAGGTGCCATCAT	4937
		ATGATGGCGACCTGGCGTCCAGAGCACGGTGAGCTCCGCGC CTTCTTCATGATCCC <u>TACCGGCCTGGAGTAGGTACACCTGCC</u> GTTGGTGGCGTTCTCGATCCGTTTATCTCAA	4938
		GCGCCGGT <u>AGGGGATCA</u>	4939
		TGATCCC <u>TACCGGC</u>	4940
20	Male-sterile AP3 <i>Triticum aestivum</i> Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG CCGGTGGGATCATGT <u>AGAAGGCGCGGAGCTACCGTGCTCT</u> GCGACGCCAGGTGCCATCATGTTCTCCT	4941
		AGGAGAACATGATGATGGCGACCTGGCGTCCAGAGCACGGTG AGCTCCCGCCCT <u>TACATGATCCCCGACCGGCCTGGAGTA</u> GGTCACCTGCCCTGGTGGCGTTCTCGATCCG	4942
		GGATCATGT <u>AGAAGGCG</u>	4943
		CGCCTTCT <u>ACATGATCC</u>	4944
25	Male-sterile Silky1 <i>Zea mays</i> Tyr21Term TAC-TAG	GGGGCGGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA ACCGCCAGGTGACCT <u>AGTCCAAGCGCCGGACGGGATCATGAAG</u> AAGGCACGGCAGCTACCGTCTGCGACGCC	4945
		GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTCATGATCC CCGTCGGCGCTTGGACTAGGTACACCTGCCGGTTGGTGGCGTTC TCGATCCGTTGATCTCGATCTGCCGCC	4946
		GTGACCT <u>AGTCCAAGCG</u>	4947
		CGCTTGGACTAGGTAC	4948

5	Male-sterile Silky1 <i>Zea mays</i> Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCCTAGCCCCGGACGGGGATCATGAAGAAGG CACCGAGCTCACCGTGCTCTGCACGCCAGG	4949
		CCTGGGCGTCGCAGAGCACGGTAGCTCGTGCCCTTCTCATG ATCCCCGTCGGCGCTAGGAGTAGGTACCTGGCGTTGGTGGC GTTCTCGATCCGCTTGTATCTCGATCTGCCGCG	4950
		CCTACTCCTAGCGCCGG	4951
		CCGGCGCTAGGAGTAGG	4952
		CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATGTAGAAGGCACCGAGCTACCGTGCTCT CCGACGCCAGGTGCCATCATCATGTTCTCCT	4953
10	Male-sterile Silky1 <i>Zea mays</i> Lys30Term AAG-TAG	AGGAGAACATGATGATGGCGACCTGGCGTGCAGAGCACGGT AGCTCGGTGCCCTCATGATCCCCGTCGGCGCTTGGAGTAG GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	4954
		GGATCATGTAGAAGGCA	4955
		TGCCTTCTACATGATCC	4956
		ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAGTAGGCACCGAGCTACCGTGCTCTGCG ACGCCAGGTGCCATCATCATGTTCTCCTCCA	4957
15	Male-sterile Silky1 <i>Zea mays</i> Lys31Term AAG-TAG	TGGAGGAGAACATGATGATGGCGACCTGGCGTGCAGAGCACG GTGAGCTCGGTGCCCTACCTCATGATCCCCGTCGGCGCTTGG GTAGGTCACCTGGCGGTTGGTGGCGTTCTCGAT	4958
		TCATGAAGTAGGCACGC	4959
		GCGTGCCTACTTCATGA	4960
		GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGGAGGGCTAGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAACGC	4961
20	Male-sterile AP3 <i>Oryza sativa</i> Lys5Term AAG-TAG	GGCGCTTCGAGTAGGTACCTGCCTGTTGGTGCCTCGATCC GCTTGATCTCGATCTAGCCCCCTCCCATGGCCGCCCGCTGCAGC AGCTATCTCTCGCCGGACAATGCAGCTAGC	4962
		GGAGGGGCTAGATCGAG	4963
		CTCGATCTAGCCCCCTCC	4964
		TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACCGCACCG ACAGGCAGGTGACCTACTCGAACCGCCGCACGG	4965
25	Male-sterile AP3 <i>Oryza sativa</i> Glu7Term GAG-TAG	CCGTGCGGGCCTCGAGTAGGTACCTGCCTGTTGGTGCCT CGATCCGCTTGTATCTGCTCGCCGGACAATGCA GCAGCAGCTATCTCTCGCCGGACAATGCA	4966
		GCAAGATCTAGATCAAG	4967
		CTTGATCTAGATCTGC	4968

5	Male-sterile AP3 <i>Oryza sativa</i> Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGA GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAAGCGCCGACGGGATCA	4969
		TGATCCCCGTGCGCGCTTCGAGTAGGTACCTGCCTGTTGGTC GCGTCTCGATCCGCTAGATCTCGATCTGCCCTCCCATGGCC	4970
		GCCCCCTGCAGCAGCTATCTCTCGCCGGAC	
		TCGAGATCTAGCGGATC	4971
		GATCCGCTAGATCTGA	4972
10	Male-sterile AP3 <i>Oryza sativa</i> Glu12Term GAG-TAG	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGA TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT ACTCGAAGCGCCGACGGGATCATGAAGAAGG	4973
		CCTTCTTCATGATCCCCGTGCGCGCTTCGAGTAGGTACCTGCC TGTTGGTCCGCGTTCTAGATCCGCTTGTCTCGATCTGCCCTCC	4974
		CCATGGCCGCCCTGCAGCAGCTATCTCTC	
		AGCGGATCTAGAACGCG	4975
		CGCGTTCTAGATCCGCT	4976

Table 15
Oligonucleotides to produce male-sterile plants

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
15	Male-sterile AG <i>Arabidopsis thaliana</i> Tyr35Term TAC-TAG	TCTGTACTAATCAAATTTCGCCCTAACGTTTGGCTTGGAGCA GCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCCCTCTCC CTTGAGGAAATCTGGGAGAGGAAAGATCGAA	4977
		TTCGATCTTCCTCTCCCAGATTCCCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAA	4978
		ACGTTAGGGCAAAATTGATTAGTACAGA	4979
		TCCGATTGCTACGCCGT	4980
20	Male-sterile AG <i>Arabidopsis thaliana</i> Gln36Term CAA-TAA	CTGTACTAATCAAATTTCGCCCTAACGTTTGGCTTGGAGCAG CAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCCCTCTCC TGAGGAAATCTGGGAGAGGAAAGATCGAA	4981
		TTTCGATCTTCCTCTCCCAGATTCCCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAA	4982
		AACGTTAGGGCAAAATTGATTAGTACAG	
		CGGCGTACTAATCGGAG	4983
25		CTCCGATTAGTACGCCG	4984

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile AG <i>Arabidopsis thaliana</i> Ser37Term TCG-TAG	ACTAATCAAATTTGCCCTAACGTTTGGCTTGAGCAGCAAT CACGGCGTACCAAT <u>AGGAGCTAGGAGGAGATTCCCTCCCTTGA</u> GGAAATCTGGGAGAGGAAGATCGAAATCAA	4985
		TTGATTTCGATCTTCCTCTCCAGATTCTCAAGGGAGAGGAAT CTCCTCCTAGCTCT <u>ATTGGTACGCCGTATTGCTGCTCCAAAGC</u> CAAAAACGTTAGGCAAAATTGATTAGT	4986
		GTACCAAT <u>AGGAGCTAG</u>	4987
		CTAGCTCC <u>ATTGGTAC</u>	4988
10	Male-sterile AG <i>Arabidopsis thaliana</i> Glu38Term GAG-TAG	TAATCAAATTTGCCCTAACGTTTGGCTTGAGCAGCAATCA CGGGCGTACCAAT <u>CGTAGCTAGGAGGAGATTCCCTCCCTTGAGGA</u> AATCTGGGAGAGGAAGATCGAAATCAAAC	4989
		GTTTGAATTCGATCTTCCTCTCCAGATTCTCAAGGGAGAGGA ATCTCCTCCTAGCT <u>ACGATTGGTACGCCGTATTGCTGCTCCAAAGC</u> GCCAAAAACGTTAGGGCAAATTGATTA	4990
		ACCAAT <u>CGTAGCTAGGA</u>	4991
		TCCTAGCT <u>ACGATTGGT</u>	4992
		CTCTCCCACITCTTTGGTGGTTATTCA <u>TTGGTACCGATATCA</u> CAGAACGCAATGG <u>ATTAAGGTGGAGTAGTCACGATGCAGAGAGTA</u> GCAAGAACGATAGGTAGAGGGAAAGATAGAGA	4993
15	Male-sterile AG <i>Brassica napus</i> Glu3Term GAA-TAA	TCTCTATCTCCCTACCTATCTCTGGTACTCTGCATCGT ACTACTCCCACCT <u>TAATCCATTGCTCTGTGATATCGTCACCAAAT</u> GAATAAACACC <u>GGAAAAGAACGATGGGAGAG</u>	4994
		CAATGGATT <u>AAAGGTGGG</u>	4995
		CCCACCT <u>TAATCCATTG</u>	4996
		TATTCA <u>TTGGTACCGATATCACAGAACGATGGATGAAGGTGGG</u> AGTAGTCACGAT <u>GCATAGAGTAGCAAGAACGATAGGTAGAGGGAAAG</u> ATAGAGATA <u>AAAGAGGATAGAGAACACAACAA</u>	4997
		TTGTTGTGTTCTATCCTCTTATCTCTATCTTCCCTACCTATC TTCTTGCTACTCT <u>ATGCATCGTACTACTCCCACCTCATCCATTG</u> CTTCTGTGATATCGTCACCAATGAATA	4998
20	Male-sterile AG <i>Brassica napus</i> Glu11Term GAG-TAG	ACGAT <u>GCATAGAGTAGC</u>	4999
		GCTACTCT <u>ATGCATCGT</u>	5000
		GGTGACGATATCACAGAACGATGGATGAAGGTGGAGTAGTCA CGAT <u>GCAGAGAGTAGCTAGAACGATAGGTAGAGGGAAAGATAGAGAT</u> AAAGAGGATAGAACACAACAA <u>ATCGTCAAG</u>	5001
		CTTGACGAT <u>TTGGTCTCTATCCTCTTATCTCTATCTTCCCT</u> CTACCTATCT <u>CTAGCTACTCTGCATCGTACTACTCCCACCTT</u> CATCCATTGCTCTGTGATATCGTCACC	5002
		AGAGTAG <u>CTAGAACGAT</u>	5003
25	Male-sterile AG <i>Brassica napus</i> Lys14Term AAG-TAG	TATCTTCT <u>AGCTACTCT</u>	5004

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile AG <i>Brassica napus</i> Lys15Term AAG-TAG	GACGATATCACAGAACATGGATGAAGGTGGGAGTAGTCACGAT GCAGAGAGTAGCAAGTAGATAGCTAGAGGGAAAGATAGAGATAAAG AGGATAGAGAACACAACAAATCGTCAAGTAA	5005
		TTACTTGACGATTGTTGTTCTATCCTCTTATCTCTATCTTC CCTCTACCTATCT <u>A</u> CTTGCTACTCTCTGCATCGTGACTACTCCAC CTTCATCCATTGCTCTGTGATATCGTC	5006
		GTAGCAAGTAGATAGGT	5007
		ACCTATCT <u>A</u> CTTGCTAC	5008
10	Male-sterile AG <i>Lycopersicon esculentum</i> Glu4Term CAA-TAA	CAACCAAAAAACTAAAAATCTTCTCTTCCCTTACAAGGTGA AGTAATGGACTT <u>C</u> TAAAGTGATCTAACCAAGAGAGATCTCACCACAA AGGAAACTAGGAAGGGGGAAAATTGAGA	5009
		TCTCAATTTCCTCCCTAGTTCCCTTGTGGTAGATCTCT GGTTAGATCACT <u>T</u> AGAAGTCCATTACTCACCTTGTAGGAAAGG AAAGAGAAGATTTAAGTTTTGGTT	5010
		TGGACTT <u>C</u> AAAGTGAT	5011
		ATCACTT <u>A</u> GAAGTCCA	5012
		AAAATCTTCTCTTCCCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAAC <u>C</u> TGAGAGATCTCACCAACAAAGGAAACTAGGAA GGGGAAAATTGAGATCAAAGGATCGAAA	5013
15	Male-sterile AG <i>Lycopersicon esculentum</i> Arg9Term AGA-TGA	TTTCGATCTTTGATCTCAATTTCCTCCCTAGTTCCCTTGT GGTGAGATCTCT <u>C</u> AGGTTAGATCACTTGGAGTCCATTACTCAC CTTGTAGGAAAGGAAAGAGAAGATTT	5014
		ATCTAAC <u>C</u> TGAGAGATC	5015
		GATCTCT <u>C</u> AGGTTAGAT	5016
		ATCTTCTCTTCCCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAACCA <u>G</u> AGATAGATCTCACCAACAAAGGAAACTAGGAAGGG GGAAAATTGAGATCAAAGGATCGAAAACA	5017
		TGTTTCGATCTTTGATCTCAATTTCCTCCCTAGTTCCCTT TGTGGTAGAGATCT <u>T</u> CTGGTTAGATCACTTGGAGTCCATTACT CACCTTGTAGGAAAGGAAAGAGAAGAT	5018
20	Male-sterile AG <i>Lycopersicon esculentum</i> Glu10Term GAG-TAG	TAACCAGATAGATCTCA	5019
		TGAGATCT <u>T</u> CTGGTTA	5020
		CTTCCCTTCCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT AACCAGAGAGATCT <u>G</u> ACCACAAAGGAAACTAGGAAGGGGGAAAAT TGAGATCAAAGGATCGAAAACACGACGAA	5021
		TTCGTCGTGTTCGATCTTGTGATCTCAATTTCCTCCCTA GTTCCCTTGTGGTCAGATCTCTGGTTAGATCACTTGGAGTC CATTACTCACCTTGTAGGAAAGGAAAG	5022
		AGAGATCT <u>G</u> ACCACAA	5023
25	Male-sterile AG <i>Lycopersicon esculentum</i> Ser12Term TCA-TGA		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		TTTGTGGTCAGATCTCT	5024
5	Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln4Term CAA-TAA	GTACTCTCATTTCAACCCCTTCTTCTTACCAAGGTGA AAGTATGGACTCTAAAGTGATCTAACAGAGAGATCTCCACAA AGGAAACTGGGAAGAGGAAAGATTGAGA	5025
		TCTCAATCTTCTTCCCAGTTCTTGTGGAGAGATCTCTCT TGTTAGATCACTTAAAGTCCATACTTACACCTGGTAAGGAAAGA AAGGGTTGGAAGATGAAAATAGAGAGTAC	5026
		TGGACTTCTAAAGTGAT	5027
		ATCACTTAAAGTCCA	5028
10	Male-sterile NAG1 <i>Nicotiana tabacum</i> Arg9Term AGA-TGA	ATCTTCCAACCCCTTCTTCTTACCAAGGTGA AAAGTGATCTAACATGAGAGATCTCTCCACAAAGGAAACTGGGAA GAGGAAAGATTGAGATCAAACGGATCGAAA	5029
		TITCGATCCGTTGATCTCAATCTTCTTCCCAGTTCTTGT GGAGAGATCTCTCATGTTAGATCACTTGGAAAGTCCATACTTCAC CTGGTAAGGAAAGAAAGGGTTGGAAGAT	5030
		ATCTAACATGAGAGATC	5031
		GATCTCTCATGTTAGAT	5032
		TTCCAACCCCTTCTTCTTACCAAGGTGA GTGATCTAACAGATAGATCTCTCCACAAAGGAAACTGGGAAAGAG GAAAGATTGAGATCAAACGGATCGAAAACA	5033
15	Male-sterile NAG1 <i>Nicotiana tabacum</i> Glu10Term GAG-TAG	TGTTTCGATCCGTTGATCTCAATCTTCTTCCCAGTTCTT TGTGGAGAGATCTATCTTGTAGATCACTTGGAAAGTCCATACTTT CACCTGGTAAGGAAAGAAAGGGTTGGAA	5034
		TAACAAGATAGATCTCT	5035
		AGAGATCTATCTTGTAA	5036
		CTTCTTACCAAGGTGA GAGAGATCTCCATAAAAGGAAACTGGGAAAGAGGAAAGATTGAGA TCAAACGGATCGAAAACACAACGAATCGTC	5037
20	Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln14Term CAA-TAA	GACGATTGGTGTGTTCGATCCGTTGATCTCAATCTTCTCT TCCCAGTTCTTAAAGGAGAGATCTCTTGTAGATCACTTGG AAGTCCATACTTACACCTGGTAAGGAAAG	5038
		TCTCTCCATAAAAGGAAA	5039
		TTTCTTAAAGGAGAGA	5040
		GCCTATGAAAACAACCCAACACGGCTGGACGCTGATGCCAA AGAAGATTGGGAAGGTGAAGAGATCGAGATCAAGCGGATCGAAAAC ACCACCAATCGTCAAGTCACCTTCTGAAAA	5041
25	Male-sterile AG <i>Rosa hybrida</i> Gly22Term GGA-TGA	TTTGCAAGGTGACTTGACCGATTGGTGGTGTGATCCGCT TGATCTCGATCTTCACTTCCCACCTTCTGATAGGC CAGGACCGTGTGGTTGTTGATAGGC	5042
		TGGGAAGGTGAAGATC	5043
		GATCTTCACTTCCCAC	5044

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile AG <i>Rosa hybrida</i> Lys23Term AAG-TAG	TATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCAAAGA AGATTGGGAAGGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTTCTGCAAAGGC	5045
		GCCTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCC GCTTGATCTCGATCT <u>A</u> TCCCCTCCCAATCTCTTGGCATCAGC GTCCAGGACCGTGTGGTTGGTTCTATA	5046
		GAAGGGGATAGATCGAG	5047
		CTCGATCT <u>A</u> TCCCCTTC	5048
		AACAAACCCAACACGGTCCTGGACGCTGATGCCAAAGAAGATTG GGAAGGGGAAAGATCTAGATCAAGCGGATCGAAAACACCACCAAT CGTCAAGTCACCTTCTGCAAAGGCGCAATG	5049
10	Male-sterile AG <i>Rosa hybrida</i> Glu25Term GAG-TAG	CATTGCGCCTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTC CGATCCGCTTGATCT <u>A</u> GATCTTCCCCTCCCAATCTCTTGGC ATCAGCGTCCAGGACCGTGTGGTTGGT	5050
		GAAAGATCT <u>A</u> GATCAAG	5051
		CTTGATCT <u>A</u> GATCTTC	5052
		CCCAACACGGTCCTGGACGCTGATGCCAAAGAAGATTGGAAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCACCAATCGTCA AGTCACCTTCTGCAAAGGCGCAATGGTTGC	5053
		GCAAACCATTGCGCCTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTTCGATCCGCT <u>A</u> GATCTCGATCTTCCCCTCCCAATCTCT TTGGGCATCAGCGTCCAGGACCGTGTGG	5054
15	Male-sterile AG <i>Rosa hybrida</i> Lys27 AAG-TAG	TCGAGATCT <u>A</u> CGGGATC	5055
		GATCCGCT <u>A</u> GATCTCGA	5056
		CAATTGCCGTTTTATTTTTCTTTTGACTAAGTAGAAATGGC GTCTCTAACGCGATT <u>A</u> ATCGACCGAGGTATCGCCCGAGAGGAAAT CGGGAGAGGAAAGATCGAGATCAAACGGA	5057
		TCCGTTGATCTCGATCTTCCCTCCGATTTCCCTCGGGCGA TACCTCGGTCGATT <u>A</u> ATCGCTTAGAGACGCCATTCTACTTAGTCA AAAAGAAAAAAAATAAAACAGGCAATTG	5058
		TAAGCGATT <u>A</u> ATCGACC	5059
20	Male-sterile far <i>Antirrhinum majus</i> Gln7Term CAA-TAA	GGTCGATT <u>A</u> ATCGCTTA	5060
		GTTTTATTTTTCTTTTGACTAAGTAGAAATGGCGTCTCTAAG CGATCAATCGACCT <u>A</u> GGTATCGCCCGAGAGGAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA	5061
		TGTTTCGATCCGTTGATCTCGATCTTCCCTCCGATTTCC CTCGGGCGATACCT <u>A</u> GGTCGATTGATCGCTTAGAGACGCCATT TACTTAGTCAAAAAGAAAAAAAATAAAAC	5062
		AATCGACCT <u>A</u> GGTATCG	5063
		CGATACCT <u>A</u> GGTCGATT	5064
25	Male-sterile far <i>Antirrhinum majus</i> Glu10Term GAG-TAG		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile far <i>Antirrhinum majus</i> Glu14Term GAG-TAG	TTTCTTTTGACTAAGTAGAAATGGCGTCTAAGCGATCAATCGA CCGAGGTATGCCCTAGAGGAAAATCGGGAGAGGAAAGATCGAG ATCAAACGGATCGAAAACAAACAAATCAAC	5065
		GTTGATTGTTGTTGATCCGTTGATCTCGATCTTCCTCTC CCGATTTCTCTA <u>AGGGCGATA</u> CTCGGTCGATTGATCGCTTAGA GACGCCATTCTACTTAGTCAAAAGAAA	5066
		TATGCCCT <u>AGAGGAA</u>	5067
		TTTCTCT <u>AGGGCGATA</u>	5068
10	Male-sterile far <i>Antirrhinum majus</i> Lys16Term AAA-TAA	TTTGACTAAGTAGAAATGGCGTCTAAGCGATCAATCGACCGAG GTATGCCCGAGAGGTAAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAACAAATCAACAGGTAA	5069
		TAACCTGTTGATTGTTGTTGATCCGTTGATCTCGATCTT CCTCTCCGATT <u>ACCTCTCGGGCGATA</u> CTCGGTCGATTGATCG CTTAGAGACGCCATTCTACTTAGTCAAA	5070
		CCGAGAGGTAAATCGGG	5071
		CCCGATT <u>ACCTCTCGG</u>	5072
		TGTCCAAGCATTATCAGTCACCACTCACAGAACATGATTAAGGAAGA AGGAAAGGGTAAGT <u>AGCAAATAAAGGGGATGTTCCAGAA</u> ATCAAGA AGAGAACATGTCAGACTCGCCTCAGAGGAA	5073
15	Male-sterile AG <i>Cucumis sativus</i> Leu21Term TTG-TAG	TTCCTCTGAGGCAGGTCTGACATCTCTCTTGATTCTGGAAACA TCCCCTTATTGCTACTTACCCCTTCTCTCTTAATCATTCTT GTGAGTGGTGA <u>CTGATAATGCTTGGACA</u>	5074
		GGGTAAGT <u>AGCAAATAA</u>	5075
		TTATTGCT <u>ACTTACCC</u>	5076
		TCCAAGCATTATCAGTCACCACTCACAGAACATGATTAAGGAAGAAG GAAAGGGTAAGT <u>GTAAATAAAGGGGATGTTCCAGAA</u> ATCAAGAAG AGAACATGTCAGACTCGCCTCAGAGGAA	5077
		TCTTCCTCTGAGGCAGGTCTGACATCTCTCTTGATTCTGGAA CATCCCCTTATT <u>ACAAC</u> TTACCCCTTCTCTCTTAATCATT TTGTGAGTGGTGA <u>CTGATAATGCTTGGACA</u>	5078
20	Male-sterile AG <i>Cucumis sativus</i> Gln22Term CAA-TAA	GTAAGTTG <u>TAATAAAG</u>	5079
		CTTTATT <u>ACAAC</u> TTAC	5080
		CATTATCAGTCACCACTCACAGAACATGATTAAGGAAGAAG GGTAAGTTG <u>CAAATAAAGGGGATGTTCCAGAA</u> ATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAAGATGGGAA	5081
		TCCCCATCTCTGAGGCAGGTCTGACATCTCTCTTGATT CTGGAACATCCCCT <u>A</u> TTTG <u>CAACTTACCC</u> TTCTCTTCTCCTTA ATCATTCTTGAGTGGTGA <u>CTGATAATG</u>	5082
		TGCAAAT <u>ATAAGGGGATG</u>	5083
25	Male-sterile AG <i>Cucumis sativus</i> Lys24Term AAG-TAG	CATCCCCT <u>A</u> TTTG <u>CAACTTACCC</u> TTCTCTTCTCCTTA	5084

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG <i>Cucumis sativus</i> Gln28Term CAG-TAG	CCACTCACAGAACATGATTAAAGGAAGAAGGAAAGGGTAAGTGCAA ATAAAGGGGATGTTCTAGAACATCAAGAACAGAGATGTCAGACTCG CCTCAGAGGAAGATGGGAAGAGGAAAGATTG	5085
	CAATCTTCCCTTCCCACCTTCTGAGGGAGTCTGACATCTT CTCTCTTGATTCTAGAACATCCCCTTATTTGCAACTTACCCCTTC CTTCTCCTTAATCATTCTGTGAGTGG	5086
	GGATGTTCTAGAACATCAA	5087
	TTGATTCTAGAACATCC	5088
Male-sterile AG <i>Zea mays</i> Cys10Term TGC-TGA	CCACCACCACCAACCACACCACACCATGCTAACATGATGACTGATC GAUTGATCTGAGCTGAGGGCGTCGTCCAAGGTCAAGGAGCAGGTGGCGAGG TGGCGGCGGCCGACGGGCTCCGGCGACAGG	5089
	CCTGTCGCCGGAGCCCGTGGCGCCGCCACCTGCTCCTTG ACCTTGGACGACGGCCCTAGCTCAGATCAGTCATCATGTTGAGC ATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	5090
	CTGAGCTGAGGGCGTC	5091
	GACGGCCCTAGCTCAG	5092
Male-sterile AG <i>Zea mays</i> Ser13Term TCG-TAG	ACCACCACCAACCACACCACACCATGCTAACATGATGACTGATC TGAGCTGCGGGCGTAGTCCAAGGTCAAGGAGCAGGTGGCGGC GGCGCCGACGGGCTCCGGCGACAGGCAGGGCA	5093
	TGCCCCTGCCCTGTCGCCGGAGCCCGTGGCGCCGCCACCT GCTCCTTGACCTGGACTACGGCCCGCAGCTCAGATCAGTCATCA TGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	5094
	CGGGCGTAGTCCAAGG	5095
	CCTTGGACTACGGCCCG	5096
Male-sterile AG <i>Zea mays</i> Lys15Term AAG-TAG	CACCAACCACCAACCACACCATGCTAACATGATGACTGATCTGAGC TGCAGGGCGTCGTCTAGGTCAAGGAGCAGGTGGCGGGCGCG CGACGGGCTCCGGCGACAGGCAGGGCAGGGGA	5097
	TCCCCCTGCCCTGCCCTGTCGCCGGAGCCCGTGGCGCCGCCCGC CACCTGCTCCTTGACCTAGGACGACGGCCCGCAGCTCAGATCAG TCATCATGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGTGGTGGT	5098
	CGTCGTCTAGGTCAAG	5099
	CTTGACCTAGGACGACG	5100
Male-sterile AG <i>Zea mays</i> Lys17Term AAG-TAG	CACCAACCACCAACCACACCATGCTAACATGATGACTGATCTGAGCTGCGGG CCGTCGTCCAAGGTCTAGGAGCAGGTGGCGGGCGGCCGACGG GCTCCGGCGACAGGCAGGGCAGGGGAGAGGCA	5101
	TGCCCTCCCCCTGCCCTGCCCTGTCGCCGGAGCCCGTGGCGC CGCCGCCACCTGCTCTAGACCTGGACGACGGCCCGCAGCTCA GATCAGTCATCATGTTGAGCATGGTGTGGTGGTGGTGGTGGT	5102
	CCAAGGTCTAGGAGCAG	5103
	CTGCTCCTAGACCTGG	5104

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile AG <i>Zea mays</i> Arg4Term CGA-TGA	TCCTACCTTTCTCCCTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATC T GAGAAGAGGAGGCTACACCATCCACAGTAA CAGGCATCATGTCGACCCCTGACTTCGGCGG	5105
		CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTCTC A GATGTGCATGCTCTGTTCTATCACACA GATTTGAGGTCTGAAGGAGAAAAGGTAGGA	5106
		TGCACATC T GAGAAGAG	5107
		CTCTCTC A GATGTGCA	5108
10	Male-sterile AG <i>Zea mays</i> Glu5Term GAA-TAA	TACCTTTCTCCCTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCGATAAGAGGAGGCTACACCATCCACAGTAACAG GCATCATGTCGACCCCTGACTTCGGCGGGC	5109
		GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTAGCCTCCTCTT A TCGGATGTGCATGCTCTGTTCTATCA CACAGATTGAGGTCTGAAGGAGAAAAGGTAA	5110
		ACATCCGATAAGAGGAG	5111
		CTCCTCTT A TCGGATGT	5112
		CTTTCTCCTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCGAGAA T AGGAGGCTACACCATCCACAGTAACAGGCA TCATGTCGACCCCTGACTTCGGCGGGGCAGC	5113
15	Male-sterile AG <i>Zea mays</i> Glu6Term GAG-TAG	GCTGCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTAGCCTCTT A TCGGATGTGCATGCTCTGTTCTA TCACACAGATTGAGGTCTGAAGGAGAAAAG	5114
		TCCGAGAA T AGGAGGCT	5115
		AGCCTCCT A TCGGAA	5116
		TTCTCCTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGC ACATCCGAGAAAGAG T AGGCTACACCATCCACAGTAACAGGCA TGTCGACCCCTGACTTCGGCGGGGCAGCAGA	5117
		TCTGCTGCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTAGCCTACTCTCTGGATGTGCATGCTCTGTTCT CTATCACACAGATTGAGGTCTGAAGGAGAA	5118
20	Male-sterile AG <i>Zea mays</i> Glu7Term GAG-TAG	GAGAAGAGTAGGCTACA	5119
		TGTAGCCTACTCTCTC	5120
		GCTGGGTCAAGGATCGTGGCGGGCGGTGGCGGGGGAGCAGC GAGAAGATGGGGAGGGGG T AGATCGAGATAAAGCGGATCGAGAA CACGACGAACCGGGCAGGTGACCTCTGCAAGCGCC	5121
		GGCGCTTGCAGAAGGTACACCTGCCGGTCTCGTGTGTTCTCGATC CGCTTATCTCGATCT A CCCCCTCCCCATCTCTGCTGCTCCCC GCCGCCACCGCCGCCGACGATCCTGACCCAGC	5122
		GGAGGGGGTAGATCGAG	5123
25	Male-sterile AG <i>Oryza sativa</i> Lys5Term AAG-TAG	CTCGATCT A CCCCCTCC	5124

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile AG <i>Oryza sativa</i> Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGCCGGGAGCAGCGAGAAGA TGGGGAGGGGGAAAGATCTAGATAAAGCGGATCGAGAACACGACG AACCAGGCAGGTGACCTTCTGCAAGCGCCGCAATG	5125
		CATTGCGGGCCTTGAGAAGGTACACCTGCCGGTCTCGTGTTC TCGATCCGCTTATCTAGATCTCCCCCTCCCCATCTTCGCTG CTCCCCGCCACCGCCGACGATCCTGA	5126
		GGAAGATCTAGATAAAG	5127
		CTTTATCTAGATCTCC	5128
10	Male-sterile AG <i>Oryza sativa</i> Lys9Term AAG-TAG	TCGTCGGCGGCGGTGGCGGCCGGGAGCAGCGAGAAGATGGGG AGGGGGAAAGATCGAGATATAGCGGATCGAGAACACGACGAACCG GCAGGGTGAACCTTCTGCAAGCGCCGCAATGGCCTC	5129
		GGAGGCCATTGCGGGCCTTGAGAAGGTACACCTGCCGGTCTCGTC GTGTTCTCGATCCGCTATATCTCGATCTCCCCCTCCCCATCTTCT CGCTGCTCCCGCCACCGCCGCCGACGA	5130
		TCGAGATATAGCGGATC	5131
		GATCCGCTATATCTCGA	5132
		GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAAG ATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGAC CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	5133
15	Male-sterile AG <i>Oryza sativa</i> Glu12Term GAG-TAG	CCTCTTCAGGAGGCCATTGCGGCCTTGAGAAGGTACACCTGC CGGTTCGTCGTGTTCTAGATCCGCTTATCTCGATCTCCCCCTC CCCATCTCTCGCTGCTCCCCGCCACCGC	5134
		AGCGGATCTAGAACACG	5135
		CGTGTCTAGATCCGCT	5136

Table 16
Oligonucleotides to produce male-sterile plants

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
20	Male-sterile PI <i>Cucumis sativus</i> Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAAT AGACAAGTTACATAGTCAGAGAGAAATGGTATCATCAAAAAAG CCAAAGAAATTACTGTTCTTGCATGCT	5137
		AGCATCGCAAAGAACAGTAATTCTTGGCTTTTGATGATACCAT TTCTTCTCTGACTATGTAATTGTCTATTGCTTGAGTTCTATTG TTTTATTTCTATTCCCTCTTCCC	5138

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile PI <i>Cucumis sativus</i> Ser22Term TCA-TGA	GTTACATA <u>G</u> CAAAGAG	5139
		CTCTTT <u>G</u> ACTATGTAAC	5140
		GAAGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAG ACAAGTTACATATT <u>G</u> AAAGAGAAGAAATGGTATCATCAAAAAAGCC AAAGAAATTACTGTTCTTGCATGCTCA	5141
		TGAGCATCGAAAGAACAGTAATTCTTGGCTTTTGATGATACC ATTTCTTCTTT <u>C</u> AATATGTAACTTGTCTATTGCTTGAGTTCTAT TCTTTTATTCTATTCCCTCTC	5142
		TACATATT <u>G</u> AAAGAGAA	5143
		TTCTCTTT <u>C</u> AATATGTA	5144
10	Male-sterile PI <i>Cucumis sativus</i> Lys23Term AAG-TAG	AGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAGAC AAGTTACATATT <u>C</u> ATAGAGAAGAAATGGTATCATCAAAAAAGCCA GAAATTACTGTTCTTGCATGCTCAAG	5145
		CTTGAGCATCGAAAGAACAGTAATTCTTGGCTTTTGATGATA CCATTCTCT <u>C</u> ATGAATATGTAACTTGTCTATTGCTTGAGTTCTC TATTCTTTTATTCTATTCCCTCT	5146
		CATATT <u>C</u> ATAGAGAAGA	5147
		TCTTCT <u>C</u> T <u>A</u> TGAATATG	5148
		GGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAGACAAG TTACATATT <u>C</u> AA <u>G</u> TAAGAAATGGTATCATCAAAAAAGCCAAGAA ATTACTGTTCTTGCATGCTCAAGTT	5149
15	Male-sterile PI <i>Cucumis sativus</i> Arg24Term AGA-TGA	AAACTTGAGCATCGAAAGAACAGTAATTCTTGGCTTTTGATG ATACCATTCTTC <u>A</u> CTTGAATATGTAACTTGTCTATTGCTTGAGTT CTCTATTCTTTTATTCTATTCCC	5150
		ATTCAA <u>A</u> GT <u>G</u> AAAGAAAT	5151
		ATTCTTC <u>A</u> CTTGAAT	5152
		GGGACGTGGGAA <u>G</u> GTGAGATCAAGAGGATTGAGAACTCAAGTAA CAGGCAGGTGACCT <u>A</u> GTCCAA <u>G</u> AGGAGGAATGGGATTATCAAGAA GGCAAAGGAGATCACTGTT <u>C</u> ATGTGATGCT	5153
		AGCATCACATAGAACAGTGATCC <u>C</u> TTGC <u>C</u> TTGATAATCCCA TTCC <u>C</u> CTCTGG <u>A</u> CTGGTCA <u>C</u> CTGC <u>C</u> TTACTTGAGTTCTCAA TCCTCTTGATCTCAAC <u>C</u> TTCCCACGTCCC	5154
20	Male-sterile PI <i>Malus domestica</i> Tyr21Term TAC-TAG	GTGACCT <u>A</u> GT <u>C</u> CAAGAG	5155
		CTCTTG <u>G</u> ACT <u>A</u> GGTCAC	5156

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile PI <i>Malus domestica</i> Lys23Term. AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG CAGGTGACCTACTCCTAGAGGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTATGTGATGCTAAAG	5157
		CTTAGCATCACATAGAACAGTGATCTCCTTGCCCTTGTATAATC CCATTCCCTCTAGAGTAGGTCACCTGCCTGTTACTTGAGTTCT	5158
		CAATCCTCTGATCTCACACCTCCCACG	
		CCTACTCCTAGAGGAGG	5159
10	Male-sterile PI <i>Malus domestica</i> Lys30Term AAG-TAG	CCTCCTCTAGAGGAGG	5160
		AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATCTAGAACAGGAAAGGAGATCACTGTTATGTG ATGCTAAAGTATCTCTTATCATTATTCTA	5161
		TAGAATAAAATGATAAGAGATACTTAGCATCACATAGAACAGTGATC TCCTTGCCTCTAGATAATCCCATTCCCTCTGGAGTAGGTCA	5162
		CCTGCCTGTTACTTGAGTTCTCAATCCT	
		GGATTATCTAGAACAGGCA	5163
15	Male-sterile PI <i>Malus domestica</i> Lys31Term AAG-TAG	TGCCTCTAGATAATCC	5164
		ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAGTAGGCACAAAGGAGATCACTGTTATGTGATG CTAAAGTATCTCTTATCATTATTCTAGCT	5165
		AGCTAGAATAAAATGATAAGAGATACTTAGCATCACATAGAACAGT GATCTCCTTGCCTACTTGATAATCCCATTCCCTCTGGAGTAG	5166
		GTCACCTGCCTGTTACTTGAGTTCTCAAT	
		TTATCAAGTAGGCACAAAG	5167
20	Male-sterile <i>globosa</i> <i>Antirrhinum majus</i> Gly2Term GGA-TGA	CTTTGCCTACTTGATAAA	5168
		CATTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAAATGTGAAGAGGAAAATTGAGATCAAAGAATTGAG AACTCAAGCAACAGGCAGGTTACTTACT	5169
		AGTAAGTAACCTGCCTGTTGCTGAGTTCTCAATTCTTTGATCTCA ATTTTCTCTTCACATTTTTGTTTTGTTTTCTCTCTGTTTG	5170
		TTTGCAGATAACTATTGAAAAATG	
		AAAAAATGTGAAGAGGA	5171
25	Male-sterile <i>globosa</i> <i>Antirrhinum majus</i> Arg3Term AGA-TGA	TCCTCTTCACATTTTT	5172
		TTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAA CAAAAAAAATGGGATGAGGAAAATTGAGATCAAAGAATTGAGAAC TCAAGCAACAGGCAGGTTACTTACTCAA	5173
		TTGAGTAAGTAACCTGCCTGTTGCTGAGTTCTCAATTCTTTGATC TCAATTCTCTCATCCCATTTTTGTTTTGTTTTCTCTCTGTT	5174
		TTTGTGAGATAACTATTGAAAA	

	Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile globosa <i>Antirrhinum majus</i> Gly4Term GGA-TGA	AAATGGGAT <u>GAGGAAAA</u>	5175
		TTTCCTCATCCCCATT	5176
		TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAA AAAATGGGAAGAT <u>GAAAAATTGAGATCAAAGAATTGAGAACTCA</u> AGCAACAGGCAGGTTACTTACTCAAAGA	5177
		TCTTGAGTAAGTAACCTGCCTGTTGAGTTCTCAATTCTTTG ATCTCAATT <u>TTTCAATCTCCCATT</u> TTTGTTTGTTTCTCTTT GTTTTGTTGCAGATAACTATTGTA	5178
		TGGGAAGAT <u>GAAAAATT</u>	5179
		AATTTTC <u>ATCTTCCCA</u>	5180
	Male-sterile globosa <i>Antirrhinum majus</i> Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAA AATGGGAAGAGG <u>ATAAAATTGAGATCAAAGAATTGAGAACTCAAGC</u> AACAGGCAGGTTACTTACTCAAAGAGAA	5181
		TTCTCTTTGAGTAAGTAACCTGCCTGTTGAGTTCTCAATTCTT TTGATCTCAATT <u>ATCCTCTCCCATT</u> TTTGTTTGTTTCTCT CTTGTGTTGTTGCAGATAACTATT	5182
		GAAGAGG <u>ATAAAATTGAG</u>	5183
		CTCAATT <u>ATCCTCTTC</u>	5184
		GCTGAGCTCTGCTGCCCTGGATCTGTTGGAGTGGAGAACGC AGTATGGGGCGCGG <u>CTAGATCAAGATCAAGAGGATCGAGAACTCT</u> ACCAACC <u>GGCAGGTGACCTCTCCAGCG</u>	5185
15	Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GGCGCTTGAGAAGGT <u>CACCTGCCGTTGGTAGAGTTCTCGATCC</u> TCTTGATCTTGAT <u>CTAGCCGCGCCC</u> ACTGCGTTCTCCACTCC CAAACAGATCCAAGGGCAGCAAGAGCTCAGC	5186
		GGCGCGG <u>CTAGATCAAG</u>	5187
		CTTGAT <u>CTAGCCGCGCC</u>	5188
		CTCTTGCTGCCCTGGATCTGTTGGAGTGGAGAACGCAGTATG GGGCGCGG <u>CAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC</u> CGGCAGGTGAC <u>CTCTCCAGCGCCGGCG</u>	5189
		CGGCCCGGCG <u>CTGGAGAAGGT</u> CACCTGCCGGTTGGTAGAGTT TCGATCCTCTTGAT <u>CTAGATCTGCGCGCCC</u> ACTGCGTTCTC CACTCCAAACAGATCCAAGGGCAGCAAGAG	5190
20	Male-sterile PI <i>Zea mays</i> Lys7Term AAG-TAG	GCAAGAT <u>CTAGATCAAG</u>	5191
		CTTGAT <u>CTAGATCTTG</u> C	5192

	Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTGGGAGTGGAGAACGGCAGTATG GGGCGCGGCAAGAT <u>T</u> AGATCAAGAGGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGCCG	5193
		CGGCCCGGCGCTTGGAGAAGGTACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGAT <u>T</u> AGATCTTGCAGCCCCATACTGCGTTCTC CACTCCAAACAGATCCAAGGGCAGCAAGAG	5194
		GCAAGAT <u>T</u> AGATCAAG	5195
		CTTGAT <u>T</u> AGATCTTGC	5196
10	Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	GATCTGTTGGGAGTGGAGAACGGCAGTATGGGGCGCGGCAAGAT CAAGATCAAGAGGGAT <u>T</u> AGAACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGGCGACTGGTCAAGAAGG	5197
		CCTTCTTGACCAGTCGGCCCGGCGCTTGGAGAAGGTACCTGC CGGTTGGTAGAGTT <u>T</u> AGATCCTCTTGATCTTGTACCTTGCAGC CCCATACTGCGTTCTCCACTCCAAACAGATC	5198
		AGAGGAT <u>T</u> AGAACTCT	5199
		AGAGTT <u>T</u> AGATCCTCT	5200
		GCTGAGCTTGTGCCCTGAATCTGTTAGGGAGTGGAGAACGG AGTATGGGGCGCGG <u>T</u> AGATCGAGATCAAGAGGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5201
15	Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GGCGCTTGGAGAAGGTACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTCGAT <u>T</u> AGCCGCGCCCCATACTCCGTTCTCCACTCC CTAACAGATTCAAGGGCAGCAAGAGCTCAGC	5202
		GGCGCGG <u>T</u> AGATCGAG	5203
		CTCGAT <u>T</u> AGCCGCGCC	5204
		CTCTTGCTGCCCTGAATCTGTTAGGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGAT <u>T</u> AGATCAAGAGGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGCCG	5205
		CGGCCCGGCGCTTGGAGAAGGTACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGAT <u>T</u> AGATCTTGCAGCCCCATACTCCGTTCTC CACTCCCTAACAGATTCAAGGGCAGCAAGAG	5206
20	Male-sterile PI <i>Zea mays</i> Glu7Term GAG-TAG	GCAAGAT <u>T</u> AGATCAAG	5207
		CTTGAT <u>T</u> AGATCTTGC	5208
		CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGCG CGGCAAGATCGAGAT <u>T</u> AGAGGGATCGAGAACTCTACCAACCGGCA GGTGACCTTCTCCAAGCGCCGGCCGGACTGG	5209
		CCAGTCCGGCCCGGCGCTTGGAGAAGGTACCTGCCGGTTGGTA GAGTTCTCGATCCT <u>T</u> AGATCTCGATCTTGCAGCCCCATACTC CGTTCTCCACTCCCTAACAGATTCAAGGGCAG	5210

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	TCGAGATCTAGAGGATC	5211
		GATCCTCTAGATCTGA	5212
		AATCTGTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CGAGATCAAGAGGATCTAGAACTCTACCAACCAGGCAAGGTGACCTT CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	5213
		CCTCTTGACCAGTCGGCCGGCGCTTGGAGAAAGGTACACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTGATCTGCCGCGC CCCATACTCCGTTCTCACTCCCTAACAGATT	5214
		AGAGGATCTAGAACTCT	5215
		AGAGTTCTAGATCCTCT	5216
	Male-sterile PI <i>Oryza sativa</i> Lys5Term AAG-TAG	TTGCTGCTAAGCTAGCTGGAGGAAGGGAGGAGGAGGAGGAGGAGG CGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGATCGAGAACT CCACCAACCGCCAGGTGACCTCTCCAAGCGCA	5217
		TGCGCTGGAGAAGGTACCTGGCGTTGGTGGAGTTCTCGATCC TCTTGATCTGATCTACCCCGCCCCATCCGCCTCCCTCCCTC CTCCTCCTCCCTCCAGCTAGCTTAGCAGCAA	5218
		GGCGCGGGTAGATCGAG	5219
		CTCGATCTACCCCGCGCC	5220
		CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGG TGGGGCGCGGGAAAGATCTAGATCAAGAGGATCGAGAACTCCACC AACCGCCAGGTGACCTCTCCAAGCGCAGGAGCG	5221
10	Male-sterile PI <i>Oryza sativa</i> Glu7Term GAG-TAG	CGCTCCTGCGCTTGGAGAAGGTACCTGGCGTTGGAGTT TCGATCCTTGTATCTAGATCTCCCGCCCCATCCGCCTCC CCTCCTCCTCCCTCCAGCTAGCTTAG	5222
		GGAAGATCTAGATCAAG	5223
		CTTGATCTAGATCTCC	5224
		TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG GCGGGAAAGATCGAGATCTAGAGGATCGAGAACTCCACCAACCGC CAGGTGACCTCTCCAAGCGCAGGAGCGGGATCC	5225
		GGATCCCGCTCCTGCGCTTGGAGAAGGTACCTGGCGTTGGT GAGTTCTGATCCTCTAGATCTGATCTCCCGCCCCATCCCG CCTCCTCCTCCCTCCAGCTAGCTAG	5226
15	Male-sterile PI <i>Oryza sativa</i> Lys9Term AAG-TAG	TCGAGATCTAGAGGATC	5227
		GATCCTCTAGATCTGA	5228

Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI <i>Oryza sativa</i>	GAAGGAGGGAGGAGGGAGGGAGGCAGGGATGGGGCGCGGGAAAGA TCGAGATCAAGAGGGAT <u>T</u> AGAAC <u>T</u> CCACCAACC <u>G</u> C <u>C</u> AGGTGACCT	5229
Glu12Term GAG-TAG	TCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGT <u>C</u> AC <u>T</u> GGC	5230
	GGTTGGTGGAG <u>T</u> CTAGATCCT <u>T</u> GAT <u>T</u> CGAT <u>T</u> CCCGGCC	
	CCATCCCGCCTCCTCC <u>T</u> CC <u>T</u> CC <u>T</u> CC <u>T</u> CC <u>T</u> TC	
	AGAGGAT <u>T</u> AGAAC <u>T</u> CC	5231
	GGAG <u>T</u> CT <u>A</u> GAT <u>C</u> CT <u>T</u>	5232

Example 7
Engineering plants for abiotic stress tolerance

Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The 5 worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing 10 levels of alcohol dehydrogenase can confer enhanced flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which 15 results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

20 The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

Table 17
Genome-Altering Oligos Conferring Stress Tolerance

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Salt Tolerance P5CS <i>Arabidopsis thaliana</i> Phe128Ala TTT-GCT	CGTCTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGTGCTAGAGATAAGGATTCAAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	5233
		TCATCCTCAGCATCGCTTGACAGTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTAGCACTGCTATCGGTACAAGCATTGAGCAACC GTCACATCCAACCTACCACACAAAAAGACG	5234
		ATAGCAGTGCTAGAGAT	5235
		ATCTCTAGCACTGCTAT	5236
10	Salt Tolerance P5CS 1 <i>Brassica napus</i> Phe128Ala TTC-GCC	GAGACTATGTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGTGCCAGAGACAAGGAGTTCAAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTGA	5237
		TCAAATCAAGCATGGACTTCACTGTCTCATTAAGTTGCTTCCTGAA CTCCTTGTCTCTGGCACTACTGTCATTCAACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	5238
		ACAGTAGTGCCAGAGAC	5239
		GTCTCTGGCACTACTGT	5240
		GAGACTATGTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGTGTCAGAGATAAGGATTCAAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAAATGA	5241
15	Salt Tolerance P5CS 2 <i>Brassica napus</i> Phe129Ala TTC-GCC	TCATTTCAGCATAGCTTGACTGTCTACTAAGTTGCTTCCTGAA ATCCTTATCTCTGACACTGCTATCAGTCACCAGCAGCTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	5242
		ATAGCAGTGCTAGAGAT	5243
		ATCTCTGACACTGCTAT	5244
		GATATGTTGTTAACCAACTGGATGTCTCGTCATCTCAACTCTTG TCACCGACAGTGATGCTGAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	5245
20	Salt Tolerance P5CS <i>Oryza sativa</i> Phe128Ala TTT-GCT	TAAGATCTAATAATGACTAACAGTTCACTGAGTTGCTCCGGAA CTTGGGTTCTCAGCATCACTGTCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTAAACAAACATATC	5246
		ACAGTGATGCTGAGAAC	5247
		GTTCTCAGCATCACTGT	5248

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Salt Tolerance P5CS <i>Medicago sativa</i> Phe128Ala TTT-GCT	GATATTTGTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTG TTACTGACAATGAT <u>GCT</u> AGAGACCAAGATTAGAAAGCAACTTC TGAAA <u>ACTGTGAGATCACTTCTAGCACTAA</u>	5249
		TTAGTGCTAGAAGTGTCTCACAGTTCAAGAAAGTTGCTTCTAA ATCTTGGCTCT <u>AGCATCATTGTCAGTAACAAGAAGCTGAGCAGAT</u> GTCACATCCAGCTGACTAAACAAAATATC	5250
		ACAATGAT <u>GCT</u> AGAGAC	5251
		GTCTCT <u>AGCATCATTGT</u>	5252
10	Salt Tolerance P5CS <i>Actinidia deliciosa</i> Phe128Ala TTT-GCT	GATACATTGTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGAT <u>GCT</u> AGGGATCCAGAATTAGGAAGCAACTTA CTGAAA <u>ACTGTAGAACATCACTATTGAATTG</u> A	5253
		TCAAATTCAATAGTGTATTCTACAGTTCAAGTAAGTTGCTTCTGAAT TCTGGATCCCT <u>AGCATCATTATCAGTAACGAGTAGCTGAGCTGAT</u> GTCACATCCAGCTGACTAAACAAATGTATC	5254
		ATAATGAT <u>GCT</u> AGGGAT	5255
		ATCCC <u>TAGCATCATTAT</u>	5256
15	Salt Tolerance P5CS <i>Cichorium intybus</i> Phe122Ala TTC-GCC	GACACACTCTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGAC <u>GCC</u> CAGAAGTCCAGAATTAGAAAACAACCTTA CTGAAA <u>ACAGTCGATTCTTATTATCTTATA</u>	5257
		TATAAGATAATAAAGAACATGACTGTTCAAGTAAGTTGTTCTAAAT TCTGGACTTCT <u>GGCGTCATTATCTGTTACAAGAAGCTGTGCTGAT</u> GTCACATCCAGTTGACTGAAGAGTGTGTC	5258
		ATAATGAC <u>GCC</u> CAGAAGT	5259
		ACTTCT <u>GGCGTCATTAT</u>	5260
20	Salt Tolerance P5CS <i>Lycopersicon esculentum</i> Phe128Ala TTT-GCT	GATTCTTGTTCAGTCAGITGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGAC <u>GCT</u> AGAGATCCAGATTAGGAGACAACCTCAA TGACACAGTAAATT <u>CGTTGCTTCTCTAA</u>	5261
		TTAGAGAAAGCAACGAATTACTGTGTCAATTGAGTTGTCCTCAA ATCTGGATCT <u>CTAGCGTCATTATCAGTCACCAGAACGCTGAGCTGA</u> TGTCA <u>CATCCAAC</u> TGACTGAACAAAGAACATC	5262
		ATAATGAC <u>GCT</u> AGAGAT	5263
		ATCT <u>CTAGCGTCATTAT</u>	5264
25	Salt Tolerance P5CS <i>Vigna unguiculata</i> Phe162Ala TTT-GCT	GATACCAGTTCAGCCAGCTTGATGTGACTTCTCCAACTTCTTG TGAATGATGGATT <u>GCT</u> AGGGATGCTGGCTCAGAAAACAACCTTC GGACACAGTGAACCGCGTATTAGATTAA	5265
		TTAAATCTAATAACCGCGTCACTGTGTCCGAAAGTTGTTCTGAA GCCAGCATCCCT <u>AGCAAATCCATCATT</u> CACAAGAACGTTGGGAAGA AGTCACATCAAGCTGGCTGAACATGGTATC	5266
		ATGGATT <u>GCT</u> AGGGAT	5267

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		ATCCCTAGCAAATCCAT	5268
5	Salt Tolerance P5CS <i>Mesembryanthemum</i> <i>crystallinum</i> Phe125Ala TTT-GCT	GACACCTTGTAGTCAGTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGAC <u>G</u> CTAGAGATCCAAGTTAGAACACAACTA ACTGAAACAGTGTATCAGTTGGATCTAA	5269
		TTAGATCCAACAACTGATACACTGTTTAGTTGTGTTCTAAA CTTGGATCTCTAGCGTCGTTGCCGTACAAGCAGCTGAGCAGCA GTCAGATCCAACGTGACTAAACAAGGTGTC	5270
		ACAACGAC <u>G</u> CTAGAGAT	5271
		ATCTCTAGCGTCGTTGT	5272
10	Salt Tolerance P5CS <i>Vitis vinifera</i> Phe130Ala TTT-GCT	GACACATTATTAAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGAT <u>G</u> CTAGGGATGAAGCTTCCGAAATCAACTTA CTCAAACAGTGGATTCTTGTTAGCTTGA	5273
		TCAAAGCTAACATGAATCCACTGTTGAGTAAGTTGATTGGAA AGCTTCATCCCTAG <u>C</u> ATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC	5274
		ATAATGAT <u>G</u> CTAGGGAT	5275
		ATCCCTAG <u>C</u> ATCATTAT	5276
15	Salt Tolerance P5CS <i>Vigna aconitifolia</i> Phe129Ala TTT-GCT	GATACGCTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGAT <u>G</u> CTCGAGATAAGGATTCAGGAAGCAGCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	5277
		TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCTGA AATCCTTATCTCGAG <u>C</u> ATCGTTATCCGTACAAGAAGCTGAGCCG ATGTCACATCGAGCTGAGTGAACACAGCGTATC	5278
		ATAACGAT <u>G</u> TCGAGAT	5279
		ATCTCGAG <u>C</u> ATCGTTAT	5280
20	Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Ser207Val TCC-GTC	AGAGATGTTCTAGTCCAAGAAATCTCACCTCTCACTTCTCCG TCTTCACAAACAGTT <u>G</u> TCACGTTGCAAACCTGGGATTTGTCCCCAC GAATGAGAACATGATCATCTTCGCAAAA	5281
		TTTGCGAAAGATGATCATGTTCTCATTGTTGGGACAAATCCGCA GTTGCAAACGT <u>A</u> CAACTGTTGTGAAGACGGAGAAAGTGAGAGG TGAGATTTCTTGGAACTAAGAACATCTCT	5282
		CAACAGTT <u>G</u> TCACGTT	5283
		AAACGTG <u>A</u> CAACTGTTG	5284
25	Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Gln237Leu CAA-CTA	CGAATGAGAACATGATCATCTTCGCAAAAACCTGGTCTCATCTG GCTCCTAATCCCTCTAGTACTGATGGGAAACACTTGTCCCTGC TTCTGGTTTGCTCATATGGGGACTTTA	5285
		TAAAGTCCCCATATGAGCAAACCAAGAAGCAAGGGAACAAAGTG TTTCCCATCAGTACTAGAGGGATTAGGAGCCAGATGAGACCAGAG TTTTGCGAAAGATGATCATGTTCTCATTG	5286

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Asn332Ser AAT-AGT	AATCCCT <u>T</u> AGTACTGA	5287
		TCAGTACTAGAGGGATT	5288
		AGTCTCTAGAAGGAATGAGTCGTACGAGAAGTTGGTGGATCGT TGTTCAAGTGGTG <u>G</u> TCGCACACACCGGAGAACTATAGTAG ACCTCTCTACACTTCCCCAGCTATCTTGGT	5289
		ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTCT CCGGTGTGTCGCG <u>A</u> CTCACCCTGAAACAACGATCCAACCAAC TTCTCGTACGA <u>C</u> TCATTCTTAGAGACT	5290
		AGTGGTG <u>A</u> GTCGCGAC	5291
		GTCGCG <u>A</u> CTCACCAC	5292
	Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Ser256Val TCG-GTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAATGGTGACCTTTCC GTCTTCACCACCG <u>T</u> GGTGACCTTTGCCAGTTGTGGGTTGTCCCG ACCAATAAA <u>C</u> ATGATTATCTTCAGCAAA	5293
		TTTGCTGAAGATAATCATGTTTCATTGGTCGGGACAAACCCACA ACTGGCAAAGGT <u>C</u> ACCACGGTGGTGAAGACGGAAAAGGTACCA TTTGAGACCTTTCTCTTTAGCACATCTCT	5294
		CCACCGTGG <u>T</u> GACCTTT	5295
		AAAGGT <u>C</u> ACCACGGTGG	5296
		CCAATGAAA <u>C</u> ATGATTATCTTCAGCAAAACTCTGGCCTCCCT GATTCTCATCCCT <u>T</u> GGCCCTTCTTGGGAACATGCTGTTCCCAC GAGCCTACGTTGACGCTTGGCTCATCGG	5297
10	Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Gln286Leu CAG-CTG	CCGATGAGCCAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCAAGAAGGG <u>C</u> CA <u>G</u> AGGGATGAGAA <u>T</u> CAGGAGGAGGCCA GAGTTTTGCTGAAGATAATCATGTTTCATTGG	5298
		CATCCCT <u>T</u> GGCCCTTC	5299
		GAAGGG <u>C</u> CA <u>G</u> AGGGATG	5300
		AATCGITGAATGGACTAAC <u>G</u> CTCCTGTGAGAAA <u>A</u> CGTGGGCCGC TGTTCA <u>G</u> TGCGTGA <u>G</u> CAGCAGACATACCGGCAGACGGTCGTC GATCTGTCCACAGTTGCTCCGCCATCTTGGT	5301
		ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACC <u>G</u> TCTC GCCGGTATGTCTGCT <u>G</u> CTCACCGACTGAAACAGCGCGCCACGA TTTCTCACAGGAG <u>C</u> TTAGTCCATTCAACGATT	5302
15	Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Asn381Ser AAC-AGC	GTGCGTG <u>A</u> G <u>C</u> AGCAGAC	5303
		GTCTGCT <u>G</u> CTCACGCAC	5304

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Salt Tolerance HKT1 <i>Oryza sativa</i> Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTCTCAT TCTCGGTACCGTC <u>G</u> TCTCGTTGCGAATGTGGGGCTCGGCCG ACAAATGAGAACATGGCAATCTTCTCCAAGA	5305
		TCTTGAGAAGAGATTGCCATGTTCTCATTTGTCGGCACGAGCCCCA CATTGCAA <u>A</u> CGAG <u>A</u> CGACC <u>G</u> TGACCGAGAATGAGAACAGTGCA ATGTTGATCCCTTCTTCAGTGGAGCTT	5306
		TCACGGTC <u>G</u> TCTCGTT	5307
		AAACGAGACGACC <u>G</u> TGA	5308
10	Salt Tolerance HKT1 <i>Oryza sativa</i> Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCC TCCTGTTCATCGGCC <u>I</u> GATTCTTGCAAGGCAATACACTTACCCCT CTTCCTAAGGCTATTGATATGGTTCTGGG	5309
		CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTA TTGCCTGCAAGAACAT <u>C</u> AGGCCGATGAACAGGAGGAGGAGGCCGG GTTCTGGAGAAGATTGCCATGTTCTCATTG	5310
		CATCGGCC <u>I</u> GATTCTTG	5311
		CAAGAACAT <u>C</u> AGGCCGATG	5312
		CAGTC <u>T</u> GTGGACTCAGCTTACCAAGAACATTCAATGCATT GTTCATGGCAGTG <u>G</u> CGCAAGGCACTCGGGGGAGAACACTCCATCG ACTGCTCACTCATGCCCTGCTGTTCTAGT	5313
15	Salt Tolerance HKT1 <i>Oryza sativa</i> Asn363Ser AAC-AGC	ACTAGAACAGCAGGGCGATGAGTGAGCAGTCGATGGAGTTCTC CCCCGAGTGCC <u>T</u> GC <u>G</u> CTCACTGCCATGAACATGCATTGATAAT CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	5314
		GGCAGTG <u>G</u> CGCAAGGC	5315
		GCCTTGCG <u>G</u> CTCACTGCC	5316
		GTGCCCACTGAACAAAGAACAGGGATCAACATCGT <u>G</u> CTTCTC TATCAGTCACCGTTG <u>T</u> CTCCTGCGAATGCAGGACTCGTGCCA CAAATGAGAACATGGCATCTTCTCAAAGAA	5317
		TTCTTGAGAACATGACCATGTTCTCATTTG <u>GG</u> CACGAGTCCT GCATT <u>CG</u> CACAGGAG <u>A</u> CAACGGT <u>G</u> ACTGATAGTGAGAACAGCAC GATGTTGATCC <u>T</u> CTGTT <u>G</u> ACTGGGGCAC	5318
20	Salt Tolerance HKT1 <i>Triticum aestivum</i> Ala240Val GCC-GTC	CACCGTT <u>G</u> CTCCTGTG CACAGGAG <u>A</u> CAACGGT <u>G</u>	5319 5320
		CAAATGAGAACATGGCATCTTCTCAAAGAACATT <u>GG</u> CCTTGT GCTGCTGAGTGG <u>C</u> TGATGCTCGCAGGCAATACATTGTTCCCT CTTCCTGAGGCTACTGGTGTGGTT <u>G</u> GG	5321
		CCCAGGAACCA <u>CC</u> AGTAGCCTCAGGAAGAGAGGGAACATGT ATTGCCTGCGAGC <u>A</u> GGCCACTCAGCAGCAACAAGAGGGCCTG AATTCTTGAGAACATGACCATGTTCTCATTG	5322
		GAGTGGCC <u>I</u> GATGCTG	5323

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Salt Tolerance HKT1 <i>Triticum aestivum</i> Asn365Ser AAT-AGT	CGAGCATCAGGCCACTC	5324
		CAGTCTTGATGGGCTCAGCTCTTACAGAAGACTGTCAATGCATT CTTCATGGTGGTGAGTGCAGGGACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCTGCCATTATAGT	5325
		ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCCTCGCACTCACCACCATGAAGAACATGACAGTC TTCTGATAAGAGCTGAGCCCACCAAAGACTG	5326
		GGTGGTGAGTGCAGGGC	5327
		GCCTCGCACTCACCACC	5328
10	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg7Term CGA-TGA	TTTTTTTGTTCGTTCAAAAACAAATCTTGAATTATGGCA ACCCGTCTTCTCTGAACAAACTTATCCGGCGATCTTACCGTTAC CCGCTTTAGCCCAGGTGGGTCCCTCCCA	5329
		TGGGAGGACCCACCGGGCTAAAAGCGGGTAACGGTAAGATCGC CGGATAAAAGTTGTTCAAGAGAACAGGGTTGCCATAAAATTCAAA GATTTTGTTCAGAACGAAAACAAAAAA	5330
		GTCTTCTCTGAACAAAC	5331
		GTTTGTTCAGAGAACAC	5332
15	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg13Term CGA-TGA	TCAAAAACAAATCTTGAATTATGGCAACCCGTCTCTCAGAA CAAACTTTATCCGGTGATCTTACCGTTACCGCTTTAGCCCGT GGGTCCCTCCACCGTGACTGCTTCCACCG	5333
		CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGC GGGTAAACGGTAAGATCACCGGATAAAAGTTGTTCTGAGAACAG GGTTGCCATAAAATTCAAAGATTGTTTGA	5334
		TTATCCGGTGATCTTAC	5335
		GTAAGATCACCGGATAA	5336
20	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Tyr15Term TAC-TAG	AAAATCTTGAATTATGGCAACCCGTCTCTCGAACAAACTTA TCCGGCGATCTTAGCGTTACCGCTTTAGCCGGTGGTCCTC CCACCGTGACTGCTTCCACCGCCGTGTC	5337
		GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACGCTAAGATGCCGGATAAAAGTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATT	5338
		CGATCTTAGCGTTACC	5339
		GGTAAACGCTAAGATCG	5340

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Leu17Term TTA-TAA	CTTGAATTATGGCAACCCGCTTCTCGAACAAACTTATCCG GCGATCTTACCGTT <u>A</u> ACCCGCTT <u>T</u> AGCCCGTGGGTCCCTCCCAC CGTACTGCTTCCACCGCCGTCGTCCCAG	5341
		TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCA CCGGGCTAAAAGCGGGT <u>I</u> AACGGTAAGATGCCGATAAAAGTTG TTCGGAGAAAGACGGTGC <u>C</u> ATAAAATTCAAAG	5342
		TTACCGTT <u>A</u> ACCCGCTT	5343
		AAGCGGGT <u>I</u> ACGGTAA	5344
10	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Gly42Term GGA-TGA	CCGGTGGGTCTCCACCGTGACTGCTCCACCGCCGTCGTCCC GGAGATTCTCTCCTT <u>T</u> GACAACAAGCACC <u>G</u> GAACCAC <u>C</u> TCTCA CAACCCAAACCCACCGAGCA <u>T</u> TCACGATG	5345
		CATCGTGAGATTGCTCGGTGGGTTGGGTGGTGAAGAGGTGGT TCCGGTGC <u>T</u> GTG <u>T</u> CAAAAGGAGAGAATCTCGGGACGACGGC GGTGGAAAGCAGTCACGGTGGGAGGACCCACCGG	5346
		TCTCCTT <u>T</u> GACAACAA	5347
		TTGTTGT <u>C</u> AAAAGGAGA	5348
15	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Arg4Term CGA-TGA	ACATGAAGCAGTGAAATCTCTGTTGTATTGAATCTTATTAGTC <u>T</u> CA AACTATGAATT <u>T</u> CGACAAGAGAA <u>G</u> AGTTGAAGGT <u>C</u> AGTGTCCAG ATTTGTCTCAT <u>G</u> AATT <u>T</u> CAAGTCGTGA	5349
		TCACGACTTAGAATT <u>C</u> ATGAGACAA <u>A</u> CTGGAAC <u>A</u> CTGAC <u>C</u> TTAC AAACTTCTTGT <u>C</u> AGAA <u>A</u> TT <u>C</u> ATAGTTGAG <u>A</u> CTAATAAGATTCAA TACAAACAGAG <u>A</u> TT <u>C</u> ACTGCTTCATGT	5350
		TGAATT <u>T</u> CGACAAGAG	5351
		CTCTGT <u>C</u> AGAA <u>A</u> TTCA	5352
20	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Gln5Term CAA-TAA	TGAAGCAGTGAAATCTCTGTTGTATTGAATCTTATTAGTC <u>C</u> AAAC TATGAATTCCG <u>A</u> TAAGAGAA <u>G</u> AGTTGAAGGT <u>C</u> AGTGTCCAGATT TGTCTCAT <u>G</u> AATT <u>T</u> CAAGTCGTGAAGC	5353
		GCTTCACGACTTAGAATT <u>C</u> ATGAGACAA <u>A</u> CTGGAAC <u>A</u> CTGAC <u>C</u> CT TACAAACTTCTT <u>A</u> TCGGAA <u>A</u> TT <u>C</u> ATAGTTGAG <u>A</u> CTAATAAGATT CAATACAAACAGAG <u>A</u> TT <u>C</u> ACTGCTTC	5354
		ATTTCCG <u>A</u> TAAGAGAG	5355
		CTTCTCTT <u>A</u> TCGGAA <u>A</u> AT	5356
25	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	AGCAGTGAAATCTCTGTTGTATTGAATCTTATTAGTC <u>C</u> AAACTAT GAATTCCG <u>A</u> CA <u>A</u> TAAGAGTTGAAGGT <u>C</u> AGTGTCCAGATTGT CTCATT <u>G</u> AATT <u>T</u> CAAGTCGTGAAG <u>C</u> TTA	5357
		TAAGCTTCACGACTTAGAATT <u>C</u> ATGAGACAA <u>A</u> CTGGAAC <u>A</u> CTGA CCTTACAA <u>A</u> CTT <u>C</u> ATT <u>G</u> TCGGAA <u>A</u> TT <u>C</u> ATAGTTGAG <u>A</u> CTAATAA GATT <u>C</u> AATACAAACAGAG <u>A</u> TT <u>C</u> ACTGCT	5358
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		TCCGACAATAGAAGTTT	5359
		AAACTTCTATTGTCGGA	5360
5	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Lys7Term AAG-TAG	AGTGAAATCTCTGTTGTATTGAATCTTATTAGTCTCAAACATGAA TTTCCGACAAGAGTAGTTGTAAAGGTCACTGTTCCAGATTGTCTC ATTGAATTCTAACAGTCGTGAAGCTTAATT	5361
		AATTAAGCTTCACGACTTAAAGATTCAATGAGACAAATCTGAAACAC TGACCTTACAAACTACTCTTGTGGAAATTCAAGTTGAGACTAA TAAGATTCAATACAAACAGAGATTCACT	5362
		GACAAGAGTAGTTGTAA	5363
		TACAAACTACTCTTGTCA	5364
		CATTGAATTCTAACAGTCGTGAAGCTTAATTGATTCTCTTCACTTTC TCGGATCAGGTTTAAAGATTGGAAGTCGGATAAGACTTCCCGA CGTGGAAATTCCCGTAAAAACGAGATTCA	5365
10	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Gln12Term CAA-TAA	GAATCTCGTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATC CGACTTCCAATCTTAAACCTGATCCGAGAAAGTGAAGAAGAAC GAATTAAAGCTTCACGACTTAGAATTCAATG TCAGGTTTAAAGATTGG	5366
		CCAATCTTAAACCTGA	5367
			5368
		TGGGAAGTCAATCCCCACGTTGAGCAGGTTGATGCATTGGCTAAA GTTATGAATCACCGCTAAAGACGAGTTGTGAGGTTTCAGGATTGG AAATCAGAGAGAAGCTCTGAGGGAAATTTC	5369
		GAAAATTCCCTCAGAGCTCTCTCTGATTCCAATCCTGAAACCT CACAAACTCGTCTTACCGGTGATTCTAACACTTAGCCAATGCATCA ACCTGCTCAACGTGGGGATTGACTTCCA ATCACCGCTAAAGACGAG	5370
15	Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln5Term CAA-TAA	CTCGTCTTACCGGTGAT	5371
			5372
		TCAATCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG AATCACCGCCAAGACTAGTTGTGAGGTTTCAGGATTGGAAATCA GAGAGAAGCTCTGAGGGAAATTTCATGCTA	5373
		TAGCATGAAAATTCCCTCAGAGCTCTCTCTGATTCCAATCCTG AAACCTCACAAACTAGTCTGGCGGTGATTCTAACACTTAGCCAAT GCATCACCTGCTAACGTGGGGATTGA	5374
		GCCAAGACTAGTTGTG	5375
20	Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gly7Term GAG-TAG	CACAAACTAGTCTTGGC	5376

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln12Term CAG-TAG	GAGCAGGGTGTGCAATTGGCTAAAGTTATGAATCACCGCCAAGAC GAGTTTGAGGTTTAGGATTGGAAATCAGAGAGAAGCTCTGAG GGAAATTTCATGCTAAAGGTGGAGTCCACC	5377
		GGTGGACTCCACCTTAGCATGAAAATTCCCTCAGAGCTCTCTC TGATTTCCAATCCTAAAACCTCACAAACTCGTCTGGCGGTGATT	5378
		TGAGGTTTAGGATTGG	5379
		CCAATCCTAAAACCTCA	5380
10	Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTGT GAGGTTTCAGGATTGTAATCAGAGAGAAGCTCTGAGGGAAATT TCATGCTAAAGGTGGAGTCCACCGAAGTAA	5381
		TTTACTTCGGTGGACTCCACCTTAGCATGAAAATTCCCTCAGAG CTTCTCTGATTACAATCCTGAAACCTCACAAACTCGTCTTGGC	5382
		GGTGATTCTAACTTAGCCAATGCATCA	5383
		CAGGATTGTAATCAGA	5384
15	Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTGT AGGTTTCAGGATTGTAATCAGAGAGAAGCTCTGAGGGAAATT CATGCTAAAGGTGGAGTCCACCGAAGTAA	5385
		CTTTACTTCGGTGGACTCCACCTTAGCATGAAAATTCCCTCAGA GCTTCTCTGATTACAATCCTGAAACCTCACAAACTCGTCTTGG	5386
		CGGTGATTCTAACTTAGCCAATGCATC	5387
		AGGATTGGTAATCAGAG	5388
20	Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Lys15Term AAA-TAA	CTCTGATTACAATCCT	5389
		CTTGAAGAATTGATCTACCACTCTAGCTGCTAACTGTTGCCCTGG TGGAGATAATGATGTAAGAGAGGACAGATATGTTAGATTCAGGA	5389
		CTGCAAATCAGAGCAATCTGTTATCTCAG	5390
		CTGAGATAACAGATTGCTCTGATTGAGTCCTGAAATCTAACATA TCTGTCCTCTTTACATCATTATCTCCACCAGGCGAACAGTTAGC	5390
25	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu2Term GAA-TAA	AGCTAAGAGTGGTAGATCAATTCTCAAG	5391
		TAATGATGTAAGAGAG	5392
30		CTCTCTTACATCATT	5392

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCCCTGGTG GAGATAATGATGGA <u>TGAGAGGACAGATATGTTAGATTCAGGAC</u> TGCAAATCAGAGCAATCTTATCTCAGAGA	5393
		TCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTGAAATCTAAC ATATCTGTCCCTCTC <u>ATTCCATCATTATCTCCACCAGGCGAACAGTT</u> AGCAGCTAAGAGTGGTAGATCAATTCTTC	5394
		TGATGGA <u>ATGAGAGGAC</u>	5395
		GTCCTCTC <u>ATTCCATCA</u>	5396
10	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu4Term GAG-TAG	GAATTGATCTACCACTCTTAGCTGCTAACTGTTGCCCTGGTGGAG ATAATGATGGA <u>AGATAGGACAGATATGTTAGATTCAGGACTGCA</u> AATCAGAGCAATCTTATCTCAGAGAACG	5397
		CGTTCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTGAAATCT AACATATCTGTCC <u>TA</u> CTTTCCATCATTATCTCCACCAGGCGAAC GTTAGCAGCTAAGAGTGGTAGATCAATT	5398
		TGGAAAG <u>ATAGGACAGA</u>	5399
		TCTGTCC <u>TA</u> CTTTCCA	5400
		ATCTACCACTCTTAGCTGCTAACTGTTGCCCTGGTGGAGATAATG ATGGAAAGAGAGG <u>ACTGATATGTTAGATTCAGGACTGCAAATCA</u> GAGCAATCTTATCTCAGAGAACGCA <u>GT</u> TT	5401
15	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg6Term AGA-TGA	AAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTG AAATCTAACATATC <u>AGT</u> CTCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAAGAGTGGTAGAT	5402
		GAGAGG <u>ACTGATATGTT</u>	5403
		AACATATC <u>AGT</u> CCCTCTC	5404
		CCACTCTTAGCTGCTAACTGTTGCCCTGGTGGAGATAATGATGGA AAGAGAGGACAGAT <u>AGGTTAGATTCAGGACTGCAAATCAGAGCA</u> ATCTTATCTCAGAGAACGCA <u>GT</u> TTACCA	5405
		TGGTAAA <u>ACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGCAG</u> TCCTGAAATCTAAC <u>CTATCTGTCCCTCTTTCCATCATTATCTCCAC</u> CAGGCGAACAGTTAGCAGCTAAGAGTGG	5406
20	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Tyr7Term TAT-TAG	GACAGATA <u>GGTTAGATT</u>	5407
		AATCTAAC <u>CTATCTGTC</u>	5408
		ATCCTTCTCTGAGAAAAAACACAGATCCGA <u>ATTTATCTTAA</u> TC GCCGGAAAA <u>ATGTAGAAAGCGATCGAGAGACAACCGCGTTCTTCT</u> TGAGCATCTCCGAC <u>CTTCTTCTTCTTCTTCTTCTT</u>	5409
25	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu2Term GAG-TAG	AAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACCGCGTTGTC TCTCGATCG <u>CTTCTACATTTTCCGGCTGATTAAGATAAAATTC</u>	5410
		GGATCTGTT <u>GGTTCTCAGAGAAGGAT</u>	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Lys3Term AAA-TAA	AAAAAATGTAGAAAGCG	5411
		CGCTTTCTACATTTTT	5412
		CTTCTCTGAGAAAAACAACAGATCCGAATTATCTTTAATCAGC CGGAAAAAATGGAGTAAGCGATCGAGAGACAACGCGTCTCTTG AGCATCTCCGACCTCTTCTTCTTCGC	5413
		GCGAAGAAGAAGAAGAAGGTGGAGATGCTCAAGAAGAACCGT TGTCTCTCGATCGTTACTCCATTTCGGCTGATTAAGATAA AATCGGATCTGTTGTTCTCAGAGAAG	5414
		AAATGGAGTAAGCGATC	5415
		GATCGCTTACTCCATT	5416
	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	GAAAAAACACAGATCCGAATTATCTTTAATCAGCCGGAAAAAA TGGAGAAAGCGATCTAGAGACAAACGCGTCTTCTTGAGCATCTCC GACCTTCTCTTCTTCTCGCACAAATTACG	5417
		CGTAATTGTGCGAAGAAGAAGAAGAGGTGGAGATGCTCAAGAA GAACGCGTTGTCTCTAGATCGCTTCTCCATTTCGGCTGATT AAAGATAAAATCGGATCTGTTGTTTC	5418
		AAGCGATCTAGAGACAA	5419
		TTGTCTCTAGATCGCTT	5420
		AAAACACAGATCCGAATTATCTTTAATCAGCCGGAAAAATGG AGAAAGCGATCGAGTAGACAACGCGTCTTCTTGAGCATCTCCGAC CTTCTCTCTTCTCGCACAAATTACGAGG	5421
10	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Arg7Term AGA-TGA	CCTCGTAATTGTGCGAAGAAGAAGAAGAGGTGGAGATGCTCAA GAAGAACCGCGTTGTCACTCGATCGCTTCTCCATTTCGGCT GATTAAGATAAAATCGGATCTGTTGTTT	5422
		CGATCGAGTAGACAACGC	5423
		GCGTTGTCACTCGATCG	5424
		ACAACAGATCCGAATTATCTTTAATCAGCCGGAAAAATGGAGA AAGCGATCGAGAGATAACGCGTCTTCTTGAGCATCTCCGACCTT CTTCTCTCTCGCACAAATTACGAGGCTT	5425
		AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAGGTGGAGATGCT CAAGAAGAACCGCGTTATCTCTCGATCGCTTCTCCATTTCGG CTGATTAAGATAAAATCGGATCTGTTGT	5426
15	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	TCGAGAGATAACCGCGTT	5427
		AACCGCGTTATCTCTCGA	5428

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Glu26Term GAA-TAA	GAGAGACAAAGAGTCTTCTGAACATCTCGTCCTCTTCTT CCTCTCACAGCTTTAAGGCTCTCTGCTTCAGCTTGCTGGC TGGGGACAGTGCTGCGTATCAGAGGACCT	5429
		AGGTCCCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAA GCAGAGAGAGAGCCTTAAAAGCTGTGAGAGGAAGAAGAAGAAGG ACGGAGATGTTCAAGAAGAACTCTTGTCTC	5430
		ACAGCTTTAAGGCTCT	5431
		AGAGCCTTAAAAGCTGT	5432
10	2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Ser32Term TCA-TGA	TTGAACATCTCCGTCCCTTCTTCTCACAGCTTGAAGG CTCTCTCTGCTTGGCTGGCTGGGACAGTGCTGCGTA TCAGAGGACCTCTCTATGGAGATGATGT	5433
		ACATCATCTCCATAGAGAGAGGTCCTGATACGCAGCACTGTCC CCAGCCAAGCAAGCTCAAGCAGAGAGAGCCTTCAAAGCTGTG AGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	5434
		CTCTGCTTGGCTT	5435
		AGCAAGCTCAAGCAGAG	5436
		TCTCCGTCCCTTCTTCTTCTCACAGCTTGAAGGCTCTC TCTGCTTCAAGCTTGGCTGGGACAGTGCTGCGTATCAGAG GACCTCTCTATGGAGATGATGTAGTCATT	5437
15	2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Cys34Term TGC-TGA	AATGACTACATCATCTCCATAGAGAGAGGTCCTGATACGCAGC ACTGTCCCCAGCCAATCAAGCTGAAGCAGAGAGAGCCTTCAA GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5438
		TCAGCTTGGCTT	5439
		CCAGCCAATCAAGCTGA	5440
		TCCGTCCCTTCTTCTTCTCACAGCTTGAAGGCTCTC TGCTTCAAGCTTGGCTAGGCTGGGACAGTGCTGCGTATCAGAGGA CCTCTCTATGGAGATGATGTAGTCATTGT	5441
20	2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Leu35Term TTG-TAG	ACAATGACTACATCATCTCCATAGAGAGAGGTCCTGATACGCA GCACTGTCCCCAGCCTAGCAAGCTGAAGCAGAGAGAGCCTC AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5442
		AGCTTGCTAGGCTGGGG	5443
		CCCCAGCCTAGCAAGCT	5444

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Tyr42Term TAT-TAG	TCACAGCTTGAAGGCTCTCTCTGCTTCAGCTTGCTGGCTGG GGACAGTGCTCGTAG <u>C</u> AGAGGGACCTCTCTATGGAGATGATGT AGTCATTGTTGCCAACATAGGACTGCACTA	5445
		TAGTCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA GAGAGAGGTCTGCTACGCAGCACTGCCCCAGCCAAGCAAG CTGAAGCAGAGAGAGAGCCTCAAAGCTGTGA	5446
		GCTGCGTAG <u>C</u> AGAGGAC	5447
		GTCCTCTGCTACGCAGC	5448
10	2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTGCTCCAGCATCTCCGCCCTTAATTCTT TTCTTCACAATT <u>A</u> GGAGTCCGCTTGCAGCAGCATACTGATGC GCAGGGGATAGCGCCGCATATCATAGGGCT	5449
		AGCCCTATGATATGCCGCGCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACT <u>C</u> TAATTGTGAGAAGAAGAATTAGAAGGGC GGAGATGCTGGAGAACACTTGCTGTCTGTTG	5450
		CACAATT <u>A</u> GGAGTCCGC	5451
		GC GGACT <u>C</u> TAATTGTG	5452
		AACAGACAGCAAGTGTGCTCCAGCATCTCCGCCCTTAATTCTT CTTCTCACAATT <u>A</u> CTAGTCCGCTTGCAGCAGCATACTGATGC CAGGGGATAGCGCCGCATATCATAGGGCT	5453
15	2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Glu26Term GAG-TAG	AAGCCCTATGATATGCCGCGCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACT <u>A</u> GTAAATTGTGAGAAGAAGAATTAGAAGGG CGGAGATGCTGGAGAACACTTGCTGTCTGTT	5454
		ACAATT <u>A</u> CTAGTCCGCT	5455
		AGCGGACT <u>A</u> GTAAATTGT	5456
		TCCAGGCATCTCCGCCCTTAATTCTTCTCACAATTACGAGTC CGCTCTTGCAGCAG <u>A</u> GTATGTGCTGCAGGGGATAGCGCCGCAT ATCATAGGGCTCTGTTATGGAGACGATGT	5457
		ACATCGTCTCCATAAAACAGAAGCCCTATGATATGCCGCGCTATCC CCTGCAGCACATACT <u>C</u> ATGCCGAAGAGCGGACTCGTAATTGTGA GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	5458
20	2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Ser32Term TCA-TGA	TGCCGCAT <u>G</u> AGTATGTG	5459
		CACATACT <u>C</u> ATGCCGA	5460

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Cys34Term TGT-TGA	TCTCCGCCCTCTAATTCTTCTCACAAATTACGAGTCCGCTCTT GCCGCATCAGTAT <u>GAGCTGCAGGGATAGCGCCGATATCATAG</u> GGCTTCTGTTATGGAGACGATGTGGTGATT	5461
		AATCACACATCGTCCATAAACAGAACGCCATGATATGCCGC GCTATCCCCTGCAGC <u>I</u> CATACTGATGCCCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	5462
		TCAGTAT <u>GAGCTGCAGG</u>	5463
		CCTGCAGC <u>I</u> CATACTGA	5464
10	2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr42Term TAT-TAG	TCACAATTACGAGTCCGCTTGCAGCATCAGTATGTGCTGCAGG GGATAGCGCCGCATAGCATAGGGCTTCTGTTATGGAGACGATGT GGTGATTGGCAGCTCATCGTACTGCACCT	5465
		AAGTGCAGTACGATGAGCTGCCAACATACCACATCGTCCATA AACAGAACCCATG <u>C</u> TATGCCGCTATCCCCTGCAGCACATAC TGATGCCAGAGAGCGGACTCGTAATTGTGA	5466
		CCCGCAT <u>AG</u> CATAGGGC	5467
		GCCCTATG <u>C</u> TATGCCG	5468
15	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Tyr22Term TAC-TAG	GAAGGCAGATCACAGGCAGAGCATTGCTACATCATCTCCGGCC TTCTTCTCCGCTTA <u>GACAAATGAATCTCGCTCTGCATCGTT</u> TGTGCAGCTGGGATAGTGCTCGTATCAA	5469
		TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCA <u>TTGTCTAAGCGGAAGAAGAAGGCCGGAGATGATG</u> TAGCAAAATGCTCTGCCCTGTTGATGCCCTTC	5470
		TCCGCTTA <u>GACAAATGA</u>	5471
		TCATTG <u>CTAAGCGGA</u>	5472
20	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTGCTACATCATCTCCGGCCTCTTCTT CCGCTTACACAAATT <u>ATATCTCGCTCTGCATCGTTGTGCAGC</u> TGGGGATAGTGCTCGTATCAAAGGACAT	5473
		ATGTCCTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATT <u>AATTGTGTAAGCGGAAGAAGAAGGCCGG</u> AGATGATGAGCAAATGCTCTGCCCTGTTGAT	5474
		ACACAA <u>ATTAAATCTCG</u>	5475
		CGAAGATT <u>AATTGTGT</u>	5476

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser27Term TCG-TAG	GGCAGAGCATTTGCTACATCATCTCCGGCCTTCTCCGCTTA CACAAATGAATCTTAGCTCTGCATCGGTTGTGCAGCTGGGA TAGTGCTTCGTATCAAAGGACATCGGTGTT	5477
		AACACCGATGTCCTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCAATTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAAATGCTCTGCC	5478
		TGAATCTTAGCTCTCTG	5479
		CAGAGAGCTAAGATTCA	5480
10	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTCCGCTTACACAAATGAATC TTCGCTCTGCATAGGTTGTGCAGCTGGGATAGTGCTTCGTA TCAAAGGACATCGGTGTTGGAGATGATGT	5481
		ACATCATCTCCAAACACCGATGTCCTTGATACGAAGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCAATTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA	5482
		CTCTGCATAGGTTGTG	5483
		CACAAACCTATGCAGAG	5484
		TCATCTCCGGCCTTCTCCGCTTACACAAATGAATCTCGCTC TCTGCATCGGTTGAGCAGCTGGGATAGTGCTTCGTATCAAAGG ACATCGGTGTTGGAGATGATGTGATT	5485
15	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Cys33Term TGT-TGA	AATCACGACATCATCTCCAAACACCGATGTCCTTGATACGAAGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCAATT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	5486
		TCGGTTTGAGCAGCTGG	5487
		CCAGCTGCTCAAACCGA	5488
		GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTCGGCTTAGGCCATGAATCTCGCTCTGCATCGGTT TGTGCAGCTGGGATAGTGCGCGTATCAA	5489
20	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Tyr22Term TAT-TAG	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCAAGCCGAAGATGAAGGCCGGAGATGAT GTAGCAGAATGCTCGCCTGTTGATTGCCTTC	5490
		TCGGCTTAGAGCCATGA	5491
		TCATGGCTCTAAGCCGA	5492

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT CGGCTTATGCCATTAAATCTCGCTCTGCATCGGTTGTGCAG CTGGGGATAGTCGCGTATCAAAGAACGT	5493
	ACGTTCTTGATACGACGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATGGCTATAAGCCGAAGATGAAGGCCGG AGATGATGAGCAGAATGCTCTGCCTGTTGAT	5494
	ATAGCCATTAAATCTTCG	5495
	CGAAGATTAAATGGCTAT	5496
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTCGGCTT ATAGCCATGAATCTTAGCTCTGCATCGGTTGTGCAGCTGGGG ATAGTGCCTCGTATCAAAGAACGTCGGTGT	5497
	AACACCGACGTTCTTGATACGACGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCAAGGCATAAGCCGAAGATGAA GGCCGGAGATGATGAGCAGAATGCTCTGCC	5498
	TGAATCTTAGCTCTCG	5499
	CAGAGAGCTAAGATTCA	5500
	TGCTACATCATCTCCGGCCTTCATCTTGGCTTATAGCCATGAATC TTCGCTCTGCATAGGTTGTGCAGCTGGGGATAGTCGCTCGTA TCAAAGAACGTCGGTGTGGAGATGATGT	5501
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Ser31Term TCG-TAG	ACATCATCTCAAACACCGACGTTCTTGATACGACGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCAAG CCGAAGATGAAGGCCGGAGATGATGTAGCA	5502
	CTCTGCATAGGTTGTG	5503
	CACAAACCTATGCAGAG	5504
	TCATCTCCGGCCTTCATCTTGGCTTATAGCCATGAATCTCGCTC TCTGCATCGGTTGAGCAGCTGGGGATAGTCGCTCGTATCAAAGA ACGTCGGTGTGGAGATGATGTCGTGATA	5505
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Cys33Term TGT-TGA	TATCACGACATCATCTCAAACACCGACGTTCTTGATACGACGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCAAG CTATAAGCCGAAGATGAAGGCCGGAGATGA	5506
	TCGGTTGAGCAGCTGG	5507
	CCAGCTGCTCAAACCGA	5508
	TCATAGTCCTTGGCCGTTGGATTCTCCAAGGTAGTGAGCTG CTATGGCAACTCATAGCAAACGCAACCTCCTCCGATTTCCCG CTCTTGGCGATGAAAATCCAGATTCCAG	5509
25 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln5Term CAG-TAG	CTGGAATCTGGGAATTTCATCGGCAAGAGCGGGAAAATCGGAAG GAGGTTGCCTTGCTAATGAGTTGCCATAGCAGCTCACTAACCTT	5510
	GGAAGAATCCAAGCGGCAAAAGAGACTATGA	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAACTCAT <u>TAGCAAACG</u>	5511
	CGTTTGCT <u>AATGAGTTG</u>	5512
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln6Term CAA-TAA	TAGTCTCTTTGCCGCTGGATTCTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAG <u>TAACGCAACCTCCGATTTCCCCTGC</u> TTGCCGATGAAAATTCCAGATTCCAGGTT AACCTGGAATCTGGGAATTTCATCGGCAAGAGCAGGGAAAATCGG AAGGAGGTTGC <u>GTTTACTGATGAGTTGCCATAGCAGCTCA</u> CTTGGAAAGAATCCAAGCGGAAAAGAGACTA CTCATCAG <u>TAACGCAA</u>	5513 5514 5515 5516
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	CTTTGCCGCTGGATTCTCCAAGGTTAGTGAGCTGCTATGCC ACTCATCAG <u>CAAACGTAACCTCCGATTTCCCCTGC</u> GATGAAAATTCCAGATTCCAGGTTCAATT AAATTGAACCTGGAATCTGGGAATTTCATCGGCAAGAGCAGGGAA AATCGGAAGGAGGTT <u>ACGTTGCTGATGAGTTGCCATAGCAGCT</u> ACTAACCTTGGAAAGAATCCAAGCGGAAAAG AGCAAACG <u>TAACCTCCT</u> AGGAGGTT <u>ACGTTGCT</u>	5517 5518 5519 5520
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAG <u>CAAACGCAACCTCCGATTT</u> CCCGCTCTGCCGAT <u>AAAATTCCAGATTCCAGGTTCAATTACA</u> CCTTCTAATCATTATTCTTAATTTCCTT AAGAAAAATTAAAGAAATAATGATTAGAAGGTGAAATTGAACCTGG AATCTGGGAATT <u>TAATCGGCAAGAGCAGGGAAAATCGGAAGGAG</u> GTTGCGTTGCTGATGAGTTGCCATAGCAGC TTGCCGAT <u>AAAATTCC</u> GGAATT <u>TAATCGGCAA</u>	5521 5522 5523 5524
2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln22Term CAG-TAG	GCAACTCATCAG <u>CAAACGCAACCTCCGATTTCCCCTGC</u> GCCGATGAAAATT <u>CCTAGATTCCAGGTTCAATTACACCTTCTAAT</u> CATTATTCTTAATTTC <u>TTGGTGGATT</u> AATCCACCAAAGAAAAATTAAAGAAATAATGATTAGAAGGTGAAATT GAACCTGGAAT <u>CTAGGAATTTCATCGGCAAGAGCAGGGAAAATCG</u> GAAGGAGGTTGC <u>GTTGCTGATGAGTTGC</u> AAAATT <u>CCTAGATTCCA</u> TGGAAT <u>CTAGGAATT</u>	5525 5526 5527 5528

Example 8**Production of albino mutants for the analysis of photosynthetic processes**

Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 18
Oligonucleotides to produce albino plants

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	White leaves Immutans <i>Arabidopsis thaliana</i> Ser5Term TCA-TGA	TTCTTCCCTGTGAAATTATCTGCTCAAATCTTGGTTCCTGACGGAG ATGGCGGCCGATT <u>GAGGCATCTCCTCTGGTACGTTGACGATTCA</u> CGGCCTTGGTTACTCTTGACGCTCTAG	5529
		CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGC <u>CTCAAATGCCGCCATCTCCGTAGGAACCAA</u>	5530
		AGATTGAGCAGATAATTACAGGAAAGAA	
		GGCGATT <u>GAGGCATCT</u>	5531
		AGATGC <u>CTCAAATGCC</u>	5532
10	White leaves Immutans <i>Arabidopsis thaliana</i> Leu12Term TTG-TAG	GCTCAAATCTTGGTTCCTGACGGAGATGGCGGCATT <u>CAGGCA</u> TCTCCTCTGGTACGT <u>A</u> GACGATT <u>CACGGC</u> TTGGTTACTCTTCG ACGCTCTAGAGCCGCCGTT <u>CGTACAGCTC</u>	5533
		GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAA GGCCGTGAAATCGT <u>TACGTACCAGAGGAGATGCCTGAAATGCC</u>	5534
		GCCATCTCCGT <u>CAGGAACCAAAGATTGAGC</u>	
		TGGTACGT <u>A</u> GACGATT	5535
		AAATCGT <u>CTACGTACCA</u>	5536
15	White leaves Immutans <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	TTGGTTCCTGACGGAGATGGCGGCATT <u>CAGGCA</u> TCTCCTCTG GTACGTTGACGATT <u>T</u> GACGGC <u>TTGGTACTCTTCGACGCTCTAG</u> AGCCGCCGTT <u>CGTACAGCTCCTCTCACCG</u>	5537
		CGGTGAGAGGAGCT <u>TACGAAACGGCGGCTCTAGAGCGTCGAAG</u> AGTAACCAAAGGCCG <u>CTCAAATCGTCAACGTACCAGAGGAGATGCC</u>	5538
		TGAAATGCCGCCATCTCCGT <u>CAGGAACCAA</u>	
		GACGATT <u>TGACGGC</u> TT	5539
		AAGGCCG <u>TCAAATCGTC</u>	5540
20	White leaves Immutans <i>Arabidopsis thaliana</i> Arg22Term CGA-TGA	GCGGCGATT <u>TCAGGCATCTCCTCTGGTACGTTGACGATT</u> CACGG CCTTGGTTACTCT <u>TGACGCTCTAGAGCCGCCGTT</u> CGTACAGCT CCTCTACCGATT <u>GCTTCATCATCTTC</u> CTC	5541
		GAGGAAGAT <u>GATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG</u> GCGGCTCTAGAGCG <u>TCAAAGAGTAACCAAAGGCCGTAAATCGTC</u>	5542
		AACGT <u>ACCGAGAGGAGATGCCTGAAATGCCGC</u>	
		TTACTCTT <u>TGACGCTCT</u>	5543
		AGAGCG <u>TCAAAGAGTAA</u>	5544
25			

5	White leaves Immutans <i>Arabidopsis thaliana</i> Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTACGGCCCTGGTTA CTCTTCGACGCTCTTGAGCCGCCGTTCGTACAGCTCTCACC GATTGCTTCATCATCTCCTCTCACC	5545	
		GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG TACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCG TGAAATCGTCAACGTACCAGAGGAGATGCCTGA	5546	
		GACGCTCTTGAGCCGCC	5547	
		GGCGGCTCAAGAGCGTC	5548	
	White leaves Immutans <i>Lycopersicon esculentum</i> Gly11Term GGA-TGA	GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTCGATT CTGCTATGAGTTTGAACCTCAGTTCTCATATTCTGTAGA GCTAGGAGTTTGAGAAGTCATCAGTT	5549	
10		AAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATGAA GAAACTGAGGTTCAAAACTCATAGCAGAAATCGAAATGCCATT TTGATCCTCTCCCTCCCACAAGAAC	5550	
		TGAGTTTGAACCTCA	5551	
		TGAGGTTCAAAACTCA	5552	
		GTGGGAAGGAAGAAGGATCAAGAATGGCGATTCGATTCTGCTA TGAGTTTGGAACCTGAGTTCTCATATTCTGTAGAGCTAGG AGTTTGAGAAGTCATCAGTTATGCAA	5553	
15	White leaves Immutans <i>Lycopersicon esculentum</i> Ser13Term TCA-TGA	TTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGA ATATGAAGAAACTCAGGTTCCAAAACTCATAGCAGAAATCGAAATC GCCATTCTGATCCTCTCCCTCCCAC	5554	
		TGGAACCTGAGTTCTT	5555	
		AAGAAACTCAGGTTCCA	5556	
		AAGAAGGATCAAGAATGGCGATTCGATTCTGCTATGAGTTGG AACCTCAGTTCTGATATTCTGTAGAGCTAGGAGTTGAGA AGTCATCAGTTATGCAATTCCCAGAA	5557	
		TTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTC TAAAACAAGAAATATCAAGAAACTGAGGTTCCAAAACTCATAGCAGA AATCGAAATGCCATTCTGATCCTCTT	5558	
20	White leaves Immutans <i>Lycopersicon esculentum</i> Ser16Term TCA-TGA	AGTTCTGATATTCTT	5559	
		AAGAATATCAAGAAACT	5560	
		AGGATCAAGAATGGCGATTCGATTCTGCTATGAGTTGGAAC TCAGTTCTCATAGCTTGTTAGAGCTAGGAGTTGAGAAGTC ATCAGTTTATGCAATTCCCAGAACCA	5561	
		TGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTA GCTCTAAAACAAGACTATGAAGAAACTGAGGTTCCAAAACTCATAG CAGAAATCGAAATGCCATTCTGATCCT	5562	
		TCTTCATAGCTTGTT	5563	
25	White leaves Immutans <i>Lycopersicon esculentum</i> Tyr17Term TAT-TAG	AAACAAGACTATGAAGA	5564	

5	White leaves Immutans <i>Lycopersicon esculentum</i> Cys19Term TGT-TGA	AAGAATGGCGATTCGATTCGCTATGAGTTTGGAACCTCAGTTCTTCATATTCTGATTAGAGCTAGGAGTTGAGAAGTCATCACTTTATGCAATTCCCAGAACCCATGTCGG	5565
		CCGACATGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAATCAAGAATATGAAGAAACTGAGGTTCCAAAAC	5566
		TCATAGCAGAAATCGAAATGCCATTCTT	
		TATTCTTGATTAGAGC	5567
		GCTCTAAATCAAGAATA	5568
10	White leaves Immutans <i>Capsicum annuum</i> Ser13Term TCA-TGA	CGCGTCCGATAAAAAAAATCAAGAATGGCGATTCATATCTGCTATGAGTTTCAACTTGCATTTCATATTCACTGCAATTCCAGCATTTTGCAATTCCAAGAACCCATTGGTTGAATTCA	5569
		GAATTCAAACAAATGGGTTCTTGAATTGCACAAAAATGCTGAATATGAAGAAGAAACTCAAGTTGCAAAACTCATAGCAGATATGGAAATCGCCATTCTGATTGGACGCG	5570
		TCGAACATTGAGTTCTT	5571
		AAGAAACTCAAGTTGCA	5572
		AAAAATCAAGAATGGCGATTCATATCTGCTATGAGTTTCAACTTCACTGTTGAAATTCTCTATTTCAGCATTTGTTGAATTCTCTATTTCAG	5573
15	White leaves Immutans <i>Capsicum annuum</i> Ser17Term TCA-TGA	AGTAAAATAGAGAATTCAAACAAATGGGTTCTTGAATTGCACA	5574
		AAAATGCTGAATATCAAGAAGAAACTGAAGTTGCAAAACTCATAGCAGATATGGAAATGCCATTCTGATTGGAAATTCTTCTGATTTCAG	
		TTCTTCTTGAATTCACTG	5575
		CTGAATATCAAGAAGAA	5576
		CAAGAATGGCGATTCATATCTGCTATGAGTTTCAACTTCAGTTCTTCATATTGAGCATTTTGCAATTCCAAGAACCCATTGGTTGAATTCTCTATTTCAGT	5577
20	White leaves Immutans <i>Capsicum annuum</i> Ser19Term TCA-TGA	TTCTTCTTCAATTGAGCATTTTGCAATTCCAAGAACCCATTGGTTGAATTGCACAAAAATGCTCAATATGAAGAAGAAACTGAAGTTGCAAAACTCATAGCAGATATGGAAATGCCATTCTGATT	5578
		TTCTTAAGTGAAAATAGAGAATTCAAACAAATGGGTTCTTGAATTGCACAAAAATGCTCAATATGAAGAAGAAACTGAAGTTGCAAAACTCATAGCAGATATGGAAATGCCATTCTGATT	
		TTCATATTGAGCATTT	5579
		AAAATGCTCAATATGAA	5580
		CGATTCATATCTGCTATGAGTTTCAACTTCAGTTCTTCATATTCACTGCAATTCCAAGAACCCATTGGTTGAATTCTCTATTTCAGT	5581
25	White leaves Immutans <i>Capsicum annuum</i> Leu21Term TTG-TAG	CTATGAGAATTCTAAGTGAAAATAGAGAATTCAAACAAATGGGTTCTTGAATTGCACAAAAATGCTCAATATGAAGAAGAAACTGAAGTTCGAAACTCATAGCAGATATGGAAATCGAGCATTTTGAATT	5582
		AGCATTTCAGTGCATT	5583
		AATTGCACTAAAATGCT	5584

5	White leaves Immutans <i>Capsicum annuum</i> Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTCGAACCTCAGTTCTTCTCATATT CAGCA <u>TTTGTA</u> AAATTCCAAGAACCCAT <u>TTGTTGAA</u> TCTCTA TTTCACCTAGGAATTCTCATAGAACT	5585
		AGTTCTATGAGAATTCTAAGTAAAAAGAGAATTCAAACAAAATG GGTTCTTGGAA <u>TTT</u> ACAAAAATGCTGAATATGAAGAAGAAACTGA AGTCGAAA <u>ACTCATAGCAGATATGGAA</u>	5586
		TTTTGT <u>GA</u> AAATTCCAA	5587
		TTGGAA <u>TTT</u> ACAAAAAA	5588
10	White leaves Immutans <i>Oryza sativa</i> Glu22Term GAG-TAG	TCGGCACGAGGGAGAAGGAGCAGACCGAGGTGCCGTGAGG AGTCCTCCCCTTCAGG <u>TAGACGGCTCCTGACGAGCCACTGG</u> TCACCGCCGAGGAGAGCTGGGTGGTAAGCTCG	5589
		CGAGCTAACCA <u>CCCAGCTCTCCTCGGCCGTGACCAGTGGCTCG</u> TCAGGAGGAGCCG <u>TCTACCTGAAGGGGAAGGACTCCTCGACGGC</u> CACCTCGGTCTGCTCCTCTCCCTCGTGGC	5590
		CCTCAGG <u>TAGACGGCT</u>	5591
		AGCCGT <u>TCTACCTGAAGG</u>	5592
		GAGCAGACCGAGG <u>GGCCGTGAGGAGTCCTCCCTCAGGGA</u> GACGGCTCCTCCTGACTAG <u>CCACTGGTCACCGCCGAGGAGAGCT</u> GGGTGG <u>TTAAGCTCGAGCAGTCCGTGAACATTT</u>	5593
15	White leaves Immutans <i>Oryza sativa</i> Glu28Term CAG-TAG	AAATGTT <u>CACGGACTGCTCGAGCTTAACCACCCAGCTCCTCGG</u> CGGTGACC <u>AGTGGCTAGTCAGGAGGAGCCGCTCCCTGAAGGGG</u> AAGGACTCCTCGACGGCAC <u>CTCGGTCTGCTC</u>	5594
		CTCCTGACT <u>AGCCACTG</u>	5595
		CAGTGG <u>CTAGTCAGGAG</u>	5596
		GTCGAGGAGTC <u>CTTCCCTTCAGGGAGACGGCTCCTGACGA</u> GCCACTGG <u>TCACCGCCTAGGAGAGCTGGGTGGTAAGCTCGAGC</u> AGTC <u>CCGTGAACATTTCC</u> TCACGGAGTCAGTCA	5597
20	White leaves Immutans <i>Oryza sativa</i> Glu34Term GAG-TAG	TGACT <u>GACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCTAA</u> CCACCCAG <u>CTCTCCTAGGCGGTGACCAGTGGCTCGTCAGGAGGA</u> GCCGT <u>TCCCTGAAGGGGAAGGACTCCTCGAC</u>	5598
		TCACCG <u>CCCTAGGAGAGC</u>	5599
		GCT <u>CTCCTAGGCGGTGA</u>	5600
		GAGGAGTC <u>CTTCCCTTCAGGGAGACGGCTCCTGACGAGCC</u> ACTGGT <u>CACCGCCGAGTAGAGCTGGGTGGTAAGCTCGAGCA</u> CCGT <u>GAACATTTCC</u> TCACGGAGTCAGTCATCA	5601
		TGAT <u>GACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCT</u> TAACCACCCAG <u>CTCTAGTCGGCGGTGACCAGTGGCTCGTCAGGA</u> GGAG <u>CCGTCTCCCTGAAGGGGAAGGACTCCTC</u>	5602
25	White leaves Immutans <i>Oryza sativa</i> Glu35Term GAG-TAG	CCGCC <u>GAGTAGAGCTGG</u>	5603
		CCAG <u>CTCTAGCGCGG</u>	5604

5	White leaves Immutans <i>Oryza sativa</i> Trp37Term TGG-TGA	CTTCCCCCTTCAGGGAGACGGCTCCTCCTGACGAGGCCACTGGTCAC CGCCGAGGAGAGCTGAGTGGTTAACGCTCGAGCAGTCCGTGAACA TTTCCTCACGGAGTCAGTCATCACGATACTT	5605
		AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTCACGGACTG CTCGAGCTTAACCAC <u>T</u> CAGCTCTCCTCGGCGGTGACCAGTGGCTC GTCAGGAGGAGCCGTCCCTGAAGGGGAAG	5606
		GAGAGCTG <u>A</u> GTGGTTAA	5607
		TTAACCA <u>T</u> CAGCTCTC	5608
		TCCGGAGGAGGAAGGGGGATTGACGAGGAGCTCACCTCGCCGCCG GCGAGGACGGCGACTGAGTCGTCAACGAGTCCCTCAAC GTATTCTCACGGATA <u>T</u> GTCA <u>T</u> TTATA <u>T</u> ACTC	5609
10	White leaves Immutans <i>Triticum aestivum</i> Trp22Term TGG-TGA	GAGTATAAAGATGACAGTATCCGTGAGGAATA <u>T</u> CGTTGAAGGACTG CTCGAAC <u>T</u> GTACG <u>A</u> CT <u>T</u> CAGTCGCCGTCC <u>T</u> CGCCGGCGAGGGTGA GCTCCTCGTCA <u>A</u> AT <u>CCC</u> CTCCTCCTCCCGGA	5610
		GGCGACTG <u>A</u> GT <u>T</u> CGTCA <u>G</u>	5611
		CTGACGACT <u>T</u> CAGTCGCC	5612
		GAGGAAGGGGGATTGACGAGGAGCTCACCTCGCCGCCGAGG ACGGCGACTGGGT <u>T</u> GT <u>T</u> GATTGAGCAGTCC <u>T</u> CAACGTATTCC TCACGGATA <u>T</u> GTCA <u>T</u> TTATA <u>T</u> ACTCGATATT	5613
		GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATA <u>T</u> CGTTGAA GGACTGCTCGA <u>A</u> AT <u>C</u> AGACGACCCAGTCGCCGTCC <u>T</u> CGCCGGCGA GGGTGAGCTCCTCGTCA <u>A</u> AT <u>CCC</u> CTCCTC	5614
15	White leaves Immutans <i>Triticum aestivum</i> Arg25Term AGA-TGA	GGGT <u>T</u> CGT <u>T</u> GATT <u>C</u> GAG	5615
		CTCGAAC <u>A</u> ACGACCC	5616
		GGGGGATTGACGAGGAGCTCACCTCGCCGCCGAGGACGGCG ACTGGGT <u>T</u> GT <u>T</u> CAGATT <u>C</u> AG <u>T</u> TC <u>A</u> ACGTATT <u>C</u> TCACGG TACT <u>T</u> GTCA <u>T</u> TTATA <u>T</u> ACTCGATATT <u>T</u> GT <u>T</u> ATC	5617
		GATA <u>C</u> AGAA <u>A</u> ATCGAGTATAAAGATGACAGTATCCGTGAGGAATA <u>T</u> GTTGAAGGACTG <u>T</u> GA <u>A</u> AT <u>T</u> GTACGACCCAGTCGCCGTCC <u>T</u> CGCC GGCGAGGGTGA <u>G</u> CTCCTCGTCA <u>A</u> AT <u>CCC</u> CC	5618
		TCAGATT <u>C</u> AG <u>T</u> CG <u>T</u> CC	5619
20	White leaves Immutans <i>Triticum aestivum</i> Glu27Term GAG-TAG	GGACTGCT <u>A</u> GA <u>A</u> AT <u>T</u> GA	5620
		GGATTGACGAGGAGCTCACCTCGCCGCCGAGGACGGCGACTG GGTCGT <u>C</u> AGATT <u>T</u> GA <u>G</u> TAG <u>T</u> CC <u>T</u> CAACGTATT <u>C</u> TCACGGATA <u>T</u> GTCAT <u>T</u> TTATA <u>T</u> ACTCGATATT <u>T</u> GT <u>T</u> ATCGT <u>G</u>	5621
		CACGATA <u>C</u> AGAA <u>A</u> ATCGAGTATAAAGATGACAGTATCCGTGAGGA TACGTTGAAGGACT <u>A</u> CT <u>C</u> GA <u>A</u> AT <u>T</u> GTACGACCCAGTCGCCGTCC <u>T</u> GCCGCCGAGGGTGA <u>G</u> CTCCTCGTCA <u>A</u> AT <u>CC</u> CC	5622
		GATT <u>C</u> GAG <u>T</u> AG <u>T</u> CC <u>T</u> TC	5623
		GAAGGACT <u>A</u> CT <u>C</u> GA <u>A</u> TC	5624
25	White leaves Immutans <i>Triticum aestivum</i> Gln28Term CAG-TAG		

5	White leaves	CGAGCAGTCCTCAACGTATTCCTCACGGATACTGTCATTTATA	5625
	Immutans	CTCGATATTCTGT <u>AGCGT</u> GACCGGGACTACGCAAGGTTCTCGTG	
	<i>Triticum aestivum</i>	CTCGAGACCATGCCAGGGTGCCTATTTC	
	Tyr46Term	GAAATAGGGCACCCCTGGCGATGGTCTCGAGCACGAAGAACCTTG	5626
	TAT-TAG	CGTAGTCGCGGT <u>CACGCT</u> TACAGAATATCGAGTATAAAGATGACAG TATCCGTGAGGAATACGTTGAAGGACTGCTCG	
		ATTCTGT <u>AGCGT</u> GACCG	5627
		CGGT <u>CACGCT</u> TACAGAAT	5628

Example 9**Altering amino acid content of plants**

Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

Table 19
Genome-Altering Oligos Conferring Amino Acid Overproduction

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Met Overproduction CGS <i>Arabidopsis thaliana</i> Arg77His CGT-CAT	TATCCTCCAGGATCTAAGATTCTCTTAATTCTGCCGTAGCT GAGCATTAAAGCCC <u>A</u> TAGAAACTGTAGCAACATCGGTGTTGCACA GATCGTGGCGGCTAAGTGGTCCAACAAACCC	5629
		GGGTTGTTGGACCCTTAGCCGCCACGATCTGTGCAACACCGAT GTTGCTACAGTTCTA <u>I</u> GGGCTTAATGCTCAGCTGACGGACGAA ATTAGGAGGAATCTAAGATCCTGGAGGATA	5630
		TAAAGCCC <u>A</u> TAGAAACT	5631
		AGTTTCTA <u>I</u> GGGCTTA	5632
10	Met Overproduction CGS <i>Arabidopsis thaliana</i> Ser81Asn AGC-AAC	TCTTAAGATTTCTCTTAATTCTGCCGTAGCTGAGCATTAAAGC CCGTAGAAACTGT <u>A</u> CAACATCGGTGTTGCACAGATCGTGGCGG CTAAGTGGTCCAACAACCCATCCTCCCGCGTT	5633
		AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTG TGCAACACCGATGTTG <u>I</u> TACAGTTCTACGGGCTTAATGCTCAGC TGACGGACGAAATTAGGAGGAATCTAAGA	5634
		AAACTGT <u>A</u> CAACATCG	5635
		CGATGTTG <u>I</u> TACAGTT	5636
		TTTCTCTTAATTCTGCCGTAGCTGAGCATTAAAGCCC <u>G</u> TAGAA ACTGTAGCAACATC <u>A</u> GTGTTGCACAGATCGTGGCGGCTAAGTGGT CCAACAACCCATCCTCCCGCGTTACCTTCGG	5637
15	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Ser GGT-AGT	CCGAAGGTAAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCC ACGATCTGTGCAACACT <u>G</u> ATGTTGCTACAGTTCTACGGGCTTAA TGCTCAGCTGACGGACGAAATTAGGAGGAA	5638
		GCAACATC <u>A</u> GTGTTGCA	5639
		TGCAACACT <u>G</u> ATGTTGC	5640
		TTCCCTCTTAATTCTGCCGTAGCTGAGCATTAAAGCCC <u>G</u> TAGAAA CTGTAGCAACATC <u>G</u> ATGTTGCACAGATCGTGGCGGCTAAGTGGTC CAACAAACCCATCCTCCCGCGTTACCTTCGGC	5641
		GCCGAAGGTAAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGC CACGATCTGTGCAACAT <u>C</u> GATGTTGCTACAGTTCTACGGGCTTAA ATGCTCAGCTGACGGACGAAATTAGGAGGAA	5642
20	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT	CAACATC <u>G</u> ATGTTGCAC	5643
		GTGCAACATCGATGTTG	5644
25	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Met Overproduction CGS <i>Fragaria vesca</i> Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC TCAGCACCAAGGCC <u>A</u> CCGCAACTGCAGAACATCGCGTCGCG CAGATCGTCGCGGCTTCGTGGTCCAACAAAGA	5645
		TCTTTGTTGGACCACGAAGCCCGACGATCTGCGCGACGCCGAT GTTGCTGCAGTTGCCG <u>T</u> GGGCCTTGGTGTGAGCTGGCGGACGA AGTTGGGAGGGAAAGCGGAGGATGAGTGACGATA	5646
		CAAGGCC <u>C</u> CCGCAACT	5647
		AGTTGCGGTGGCCTTG	5648
10	Met Overproduction CGS <i>Fragaria vesca</i> Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAG GCCCGCCGCAACTGCA <u>A</u> CAACATCGCGTCGCGCAGATCGTCG GGCTTCGTGGTCCAACAAAGACTCCGACCTTC	5649
		GAAAGGTGGAGTCTTGTGACCACGAAGCCCGACGATCTG CGCGACGCCGATGTTG <u>T</u> GCAGTTGCCGCGGGCCTTGGTGTGA GCTGGCGGACGAAGTTGGGAGGGAAAGCGGAGGA	5650
		CAACTGCA <u>A</u> CAACATCG	5651
		CGATGTTG <u>T</u> GCAGTTG	5652
		TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG CAACTGCAACAT <u>C</u> AGCGTCGCGCAGATCGTCGCGGCTTCGT GGTCCAACAAAGACTCCGACCTTCGGCGGTGC	5653
15	Met Overproduction CGS <i>Fragaria vesca</i> Gly80Ser GGC-AGC	GCACCGCCGAAAGGTGGAGTCTTGTGACCACGAAGCCCG ACGATCTGCGCGACG <u>C</u> TGATGTTGCTGCAGTTGCCGCGGGCCT GGTGTGAGCTGGCGGACGAAGTTGGGAGGGAA	5654
		GCAACAT <u>C</u> AGCGTCGCG	5655
		CGCGACGC <u>T</u> GATGTTGC	5656
		TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG AACTGCAACAT <u>C</u> AGCGTCGCGCAGATCGTCGCGGCTTCGT GTCCAACAAAGACTCCGACCTTCGGCGGTGC	5657
20	Met Overproduction CGS <i>Fragaria vesca</i> Gly80Asp GGC-GAC	GGCACCGCCGAAAGGTGGAGTCTTGTGACCACGAAGCCCG GACGATCTGCGCGACG <u>C</u> CGATGTTGCTGCAGTTGCCGCGGGCCT TGGTGTGAGCTGGCGGACGAAGTTGGGAGGGAA	5658
		CAACAT <u>C</u> AGCGTCGCGC	5659
		GCGCGACG <u>T</u> CGATGTTG	5660
		TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCAGGCCAGC TAAGCACCAAGGC <u>G</u> AGGCCAACTGCAGAACATCGCGTCGCG CAAATCGTCGCCGCTTCGTGGTCAACAAACAG	5661
25	Met Overproduction CGS <i>Glycine max</i> Arg68His CGC-CAC	CTGTTGTCGACCACGAAGCGCGACGATTTGCAGCGACGCCGAT GTTGCTGCAGTTGCCG <u>C</u> TGCCCTGGTGTAGCTGGCGCTGGA AGTTGGGAGGGAAAGCGGAGGATGAGGGAGGAGA	5662
		CCAAGGC <u>G</u> AGGCCGAAC	5663

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		GTTGCGGC <u>T</u> CGCCTTGG	5664
5	Met Overproduction CGS <i>Glycine max</i> Ser72Asn AGC-AAC	TCCCTCCGCTCCCTCCCAACTTCCAGCGCCAGCTAACGCACCAAG GCGCGCCGCAACTGCA <u>A</u> CAACATCGGCGTCGCGCAAATCGTCGC CGCTTCGTGGTCGAACAACAGCGACA <u>A</u> CTCTCC	5665
		GGAGAGTTGTCGCTTGTGACCACGAAGCGGCAGCATTG CGCGACGCCGATGTTGTCAGTTGCAGTGCAGCAGCCTTGGTGCTTA GCTGGCGCTGGAAGTTGGGAGGGAAAGCGGAGGA	5666
		CAACTGCA <u>A</u> CAACATCG	5667
		CGATGTTG <u>T</u> TCAGTTG	5668
10	Met Overproduction CGS <i>Glycine max</i> Gly75Ser GGC-AGC	TTCCCTCCCAACTTCCAGCGCCAGCTAACGCACCAAGGCAGCGCCG CAACTGCAACAT <u>C</u> AGCGTCGCGCAAATCGTCGCCGCTTCGT GGTCGAACAACAGCGACA <u>A</u> CTCTCCGGCCGCG	5669
		CGGCGGCCGGAGAGTTGTCGCTTGTGACCACGAAGCGGC GACGATTGCGCAGC <u>T</u> GATGTTGCTGCAGTTGCAGCAGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	5670
		GCAACAT <u>C</u> AGCGTCGCG	5671
		CGCGACG <u>T</u> CGATGTTG	5672
		TCCCTCCCAACTTCCAGCGCCAGCTAACGCACCAAGGCAGCGCCG AACTGCAACAT <u>C</u> AGCGTCGCGCAAATCGTCGCCGCTTCGT GTCGAACAACAGCGACA <u>A</u> CTCTCCGGCCGCG	5673
15	Met Overproduction CGS <i>Glycine max</i> Gly75Asp GGC-GAC	CGGCGGCCGGAGAGTTGTCGCTTGTGACCACGAAGCGGC GACGATTGCGCAGC <u>T</u> GATGTTGCTGCAGTTGCAGCAGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	5674
		CAACAT <u>C</u> AGCGTCGCG	5675
		CGCGACG <u>T</u> CGATGTTG	5676
		TGTCTTCTGTATTTCAAGGTTCCCTCTAATTCTGAGGCAGCT .AAGCATTAAGGCT <u>C</u> ACAGGAATTGCAGCAATATTGGCGTGGCTCA AGTTGTGGCGCTCCCTGGTCTAACACCA	5677
		TGGTTGTTAGACCAGGAAGCCGCCACA <u>A</u> CTTGAGCCACGCCAATA TTGCTGCAATTCTGT <u>G</u> AGCCTTAATGCTAGCTGCCCTACGAAAT TAGGAGGAAACCTGAAAATCAGAGAAGACA	5678
20	Met Overproduction CGS <i>Solanum tuberosum</i> Arg70His AGG-CAC	TAAGGCT <u>C</u> ACAGGAATT	5679
		AATTCC <u>T</u> GTGAGCCTTA	5680
		TTTCAGGTTCCCTCTAATTCTGAGGCAGCTAACGATTAAGGC TAGGAGGAATTGCA <u>A</u> CAATATTGGCGTGGCTCAAGTTGTGGCG CTTCCTGGCTAACACCAAGCCGGCTCTGA	5681
		TCAGGACCGGCTTGGTTG <u>T</u> AGACCAGGAAGCCGCCACA <u>A</u> CTG AGCCACGCCAATATTG <u>T</u> TCAGCAATTCCCTCTAGCCTTAATGCTTAGC TGCCTCACGAAATTAGGAGGAAACCTGAAAA	5682
25	Met Overproduction CGS <i>Solanum tuberosum</i> Ser74Asn AGC-AAC		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Ser GGC-AGC	GAATTGCAACAATATTG	5683
		CAATATTG <u>T</u> GCAATT	5684
		TTCCTCCTAATTCGTGAGGCAGCTAACGATTAAGGCTAGGAGG AATTGCAGCAATATT <u>A</u> CGTGGCTAACGTTGTGGCGCTTCCTGG TCTAACAAACCAAGCCGGTCCTGAATTCACTC	5685
		GAGTGAATTCAAGGACCGGCTTGGTTAGACCAGGAAGCCGC ACAACTTGAGCCACG <u>C</u> TAATATTGCTGCAATTCTCCTAGCCTAA TGCTTAGCTGCCTCACGAAATTAGGAGGAAA	5686
		GCAATATT <u>A</u> CGTGGCT	5687
		AGCCACG <u>C</u> TAATATTGC	5688
	Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Asp GGC-GAC	TTCCTCCTAATTCGTGAGGCAGCTAACGATTAAGGCTAGGAGGA ATTGCAGCAATATT <u>G</u> ACGTGGCTAACGTTGTGGCGCTTCCTGGT CTAACAAACCAAGCCGGTCCTGAATTCACTCC	5689
		GGAGTGAATTCAAGGACCGGCTTGGTTAGACCAGGAAGCCGC CACAACTTGAGCCACG <u>T</u> CAATATTGCTGCAATTCTCCTAGCCTA ATGCTTAGCTGCCTCACGAAATTAGGAGGAA	5690
		CAATATT <u>G</u> ACGTGGCTC	5691
		GAGCCACG <u>T</u> CAATATTG	5692
		CTTCCTCTTATCCCTCGCTTCCCTCCAACTTTGTCCGTCAAGCT CAGCACCAAGGCTGCC <u>A</u> CAACTGCAACATTGGTGTGCCAC AGGTGCTCGCTGCCCTGGTCCAACAACTC	5693
10	Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Arg73His CGC-CAC	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTG <u>T</u> GGCGAGCCTTGGTCTGAGCTGACGGACAA AGTTGGGAGGAAAGCGAAGGATAAGAGAGAGGAAG	5694
		GGCTCGCC <u>A</u> CAACTGCA	5695
		TGCAGTTG <u>T</u> GGCGAGCC	5696
		TCCTTCGCTTCCCTCCAACTTTGTCCGTCA <u>G</u> CTCAGCACCAAGG CTCGCCGCAACTGCA <u>A</u> CAACATTGGTGTGCACAGGTGTCGCT GCCTCCTGGTCCAACAAACTCCGATGCCGGCGC	5697
		GCGCCGGCATGGAGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTG <u>T</u> GCAGTTGCGGGAGCCTTGGTCTG AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA	5698
15	Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Ser77Asn AGC-AAC	CAACTGCA <u>A</u> CAACATTG	5699
		CAATGTTG <u>T</u> GCAGTTG	5700

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Gly80Ser GGT-AGT	TTCCCTCCCAACTTGTCCGTAGCTCAGCACCAAGGCTGCCGC AACTGCAGCAACATT <u>A</u> GTGTCGCACAGGTCGTGCTGCCCTTG GTCCAACA <u>A</u> CTCCGATGCCGGGCCACCTCTT	5701
		AAGAGGTGGCGCCGGCATCGGAGTTGGACCAGGAGGCAGC GACGACCTGTGCGACACTAATGTTGCTGCAGTTGGGGAGGAAA	5702
		GCAACATT <u>A</u> GTGTCGA	5703
		TGGGACTGAGCTGACGGACAAAGTTGGGAGGAAA	5704
10	Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Gly80Asp GGT-GAT	TTCCCTCCCAACTTGTCCGTAGCTCAGCACCAAGGCTGCCGCA ACTGCAGCAACATT <u>G</u> ATGTCGCACAGGTCGTGCTGCCCTTG TCCAACA <u>A</u> CTCCGATGCCGGGCCACCTCTT	5705
		CAAGAGGTGGCGCCGGCATCGGAGTTGGACCAGGAGGCAG CGACGACCTGTGCGACATCAATGTTGCTGCAGTTGGCGAGCC	5706
		TTGGTGGCTGAGCTGACGGACAAAGTTGGGAGGAAA	
		CAACATT <u>G</u> ATGTCGAC	5707
15	Met Overproduction CGS <i>Zea mays</i> Arg41His CGC-CAC	GTGCGACAC <u>A</u> CAATGTTG	5708
		CCTCTGCTACCATCCCTCGCTTCCGCCAAACTTGTCCGCCAGC TTAGCACCAAGGCAC <u>A</u> CCGCAACTGCAGCAACATGGCGTCGCG CAGATCGTCGCCGCCGTGGTCCGACTGCC	5709
		GGGCAGTCGGACCACGCCGGCGACGATCTGCCGACGCCGA TGTTGCTGCAGTTGGG <u>T</u> GTGCCCTGGTCTAAGCTGGCGAAC	5710
		AAGTTGGCGGAAAGCGGAGGATGGTAGCAGAGG	
		CAAGGCAC <u>A</u> CCGCAACT	5711
20	Met Overproduction CGS <i>Zea mays</i> Ser45Asn AGC-AAC	AGTTGCGGG <u>T</u> GTGCCCTTG	5712
		TCCTCCGCTTCCGCCAAACTTGTCCGCCAGCTAGCACCAAGG CACGCCGCAACTGC <u>A</u> CAACATCGCGTCGCGAGATCGCC GCCCGCGTGGTCCGACTGCCCGCCGCTGCC	5713
		GGGCGAGCGGCGGGGCAGTCGGACCACGCCGGCGACGATC TGCGCGACGCCGATGTTG <u>T</u> GCAGTTGGCGTGCCTGGTCT	5714
		AAGCTGGCGGACAAAGTTGGCGGAAAGCGGAGGA	
		CAACTGCA <u>A</u> CAACATCG	5715
25	Met Overproduction CGS <i>Zea mays</i> Gly48Ser GGC-AGC	CGATGTT <u>T</u> GCAGTTG	5716
		TTTCGCCAAACTTGTCCGCCAGCTAGCACCAAGGCACGCCGC AACTGCAGCAACAT <u>C</u> AGCGTCGCGCAGATCGCCGCCCGCGTG GTCGACTGCCCGCCGCTGCC	5717
		CTAAGTGGGGCGAGCGGCGGGCAGTCGGACCACGCCGG CGACGATCTGCGCAGC <u>G</u> CTGATGTTGCTGCAGTTGGCGTGC TTGGTGGCTAAGCTGGCGGACAAAGTTGGCGGAAA	5718
		GCAACATCAGCGTCGCG	5719

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Met Overproduction CGS <i>Zea mays</i> Gly48Asp GGC-GAC	CGCGACGC <u>T</u> GATGTTGC	5720
		TTCCGCCAAACTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCG <u>A</u> CGTCGCCAGATCGTCGCCGCCGTG GTCCGACTGCCGCCGCTGCCCGACTTAGG	5721
		CCTAAGTGGGGCGAGCGGGGGCAGTCGGACCACGGCG GCGACGATCTGCGCAGC <u>G</u> CGATGTTGCTGCAGTTGCCGTGC CTTGGTCTAACGCTGGCGAACAAAGTTGGCGAA	5722
		CAACATCG <u>A</u> CGTCGCC	5723
		GCGCGACG <u>T</u> CGATGTTG	5724
10	Met Overproduction TS <i>Arabidopsis thaliana</i> Leu205Arg CTT-CGT	GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATAACAG GAAGTTCAAGGATCG <u>T</u> GAATGACTGTTGGTAGTCAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT	5725
		ACCACAGGTCGTTCATCTTCTCAGACGATTAACCTGACTAACCA AAACAGTCATTCCAC <u>G</u> ATCCTTGAACACTTCCTGTATGACTAACCC ACAGTGTTCACCCACAGATCATTAC	5726
		CAAGGATCG <u>T</u> GGAAATGA	5727
		TCATTCCAC <u>G</u> ATCCTTG	5728
		GCATGACTGATTTGTGGGCAAACACTGTGGGATTAGCCATACTG GTAGTTAAGGATCG <u>T</u> GGGATGACTGTTGGTAGTCAGTTAA TCGCTTGCAGAAAATGCATAAACCGGGTTG	5729
15	Met Overproduction TS <i>Solanum tuberosum</i> Leu198Arg CTT-CGT	ACAACCGGTTATGCATTTCCGCAAGCGATTAACCTGACTCACCA AAACAGTCATCCCAC <u>G</u> ATCCTAAAACCTACCAAGTATGGCTAACCC ACAGTGTTCACCCACAAATCAGTCATGC	5730
		TAAGGATCG <u>T</u> GGGATGA	5731
		TCATCCCAC <u>G</u> ATCCTTA	5732
		TCATTGGGCACACAGTGA <u>ACT</u> GCTTGGCTCTAGAACAAAGTGA TAGGCAACACAGGAA <u>A</u> CAACTCAACCAGAGAACCGTCCACGCA ACAGAACAGGGATTGCTGTTGGCATGCATGC	5733
		GCATGCATGCCAACAGCAA <u>AT</u> CCCTGTTCTGTTGGACGGCT TCTCTGGTTGAGTTG <u>T</u> TCCTGTGTTGCCATCACTTGATTCTAG AGCCAAGCAGTTCACTGTGTGCCAACATGA	5734
20	Lys Overproduction DHPS <i>Zea mays</i> Ser157Asn AGC-AAC	CACAGGAA <u>A</u> CAACTCAA	5735
		TTGAGTTG <u>T</u> TCCTGTG	5736
		GCTCTAGAACAAAGTGA <u>AGG</u> CAACACAGGAAGCA <u>ACT</u> CAACCA GAGAACCGTCCAC <u>G</u> AAACAGAACAGGGATTGCTGTTGGCATG	5737
		CATGCCGTCTCCACATCAATCCTACTACGG	
		CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC AAATCCCTGTTCTGTT <u>C</u> GTGGACGGCTCTGGTTGAGTTGCTT CCTGTGTTGCCATCACTTGATTCTAGAGC	5738
25	Lys Overproduction DHPS <i>Zea mays</i> Ala166Val GCA-GAA		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGTCCACG <u>A</u> ACAGAAC	5739
	GTTCTG <u>T</u> CGTGGACG	5740
5 Lys Overproduction DHPS <i>Zea mays</i> Ala166Thr GCA-ACA	GGCTCTAGAACAA <u>G</u> TGATAGGCAACACAGGAAGCAACTCAACC AGAGAAGCCGTCCAC <u>C</u> ACAACAGAACAGGGATTGCTGTTGGCAT GCATGCGGCTCTCCACATCAATCCTTACTACG	5741
	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCCAACAGCAA ATCCC <u>T</u> GTTCTGTTG <u>T</u> GTGGACGGCTCTGGTTGAGTTGCTTC CTGTGTTGCCTATCACTTGATTCTAGAGCC	5742
	CCGTCCAC <u>A</u> CAACAGAA	5743
	TTCTGTTG <u>T</u> GTGGACGG	5744
10 Lys Overproduction DHPS <i>Oryza sativa</i> Ser124Asn AGT-AAT	TTATTGGGCATACAG <u>T</u> AACTGCTTGGCACTAAA <u>A</u> TTAAAGTGGT CGGCAACACAGGA <u>A</u> TA <u>CT</u> CAACAA <u>GG</u> GGAGGCTATT <u>CG</u> CAAC TGAGCAGGGATT <u>CG</u> CTGTAGGTATGCACGC	5745
	GCGTGCATACCTACAG <u>CG</u> AA <u>T</u> CCCTGCTCAGTGC <u>GT</u> GAATAGCC TCCCTGTTGAGTT <u>A</u> TT <u>CC</u> CTGTTGCCGACC <u>CT</u> TA <u>TT</u> AGT GCCAA <u>AG</u> CAG <u>TT</u> ACT <u>GT</u> TATGCCAATAA	5746
	CACAGGA <u>A</u> TA <u>CT</u> CAA	5747
	TTGAG <u>TT</u> A <u>TT</u> CC <u>CT</u> GTG	5748
15 Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Val GCA-GTA	GC <u>ACT</u> AAA <u>A</u> TTAA <u>AG</u> TGG <u>CG</u> CAACACAGGAAG <u>TA</u> CT <u>CA</u> ACAA GGG <u>AGG</u> CTATT <u>CA</u> CG <u>TA</u> CT <u>GA</u> GC <u>AG</u> GG <u>AT</u> TC <u>GT</u> GTAG <u>GT</u> AT <u>GC</u> CAC <u>GC</u> GG <u>CT</u> CT <u>CC</u> ACAT <u>CA</u> AT <u>CC</u> TT <u>AC</u> AC <u>GG</u>	5749
	CCGTAGTAAGGATTGATGTGGAGAGCCGC <u>GT</u> GC <u>AT</u> AC <u>CT</u> AC <u>AG</u> GA <u>AT</u> CC <u>CT</u> G <u>CT</u> CAG <u>TT</u> <u>AC</u> GT <u>GA</u> AT <u>AG</u> C <u>CT</u> CC <u>CT</u> G <u>TT</u> G <u>AG</u> <u>TT</u> <u>AC</u> CCTGTGTTGCCGACC <u>AC</u> <u>TT</u> AA <u>TT</u> AG <u>GT</u> <u>GC</u>	5750
	TATT <u>CA</u> CG <u>TA</u> CT <u>GA</u> <u>GC</u>	5751
	GCT <u>CA</u> GT <u>TT</u> <u>AC</u> GT <u>GA</u> ATA	5752
20 Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Thr GCA-ACA	GGC <u>ACT</u> AAA <u>A</u> TTAA <u>AG</u> TGG <u>CG</u> CAACACAGGAAG <u>TA</u> CT <u>CA</u> ACAA AGGG <u>AGG</u> CTATT <u>CA</u> CA <u>CT</u> <u>GA</u> CT <u>GA</u> GC <u>AG</u> GG <u>AT</u> TC <u>GT</u> GTAG <u>GT</u> GC <u>AC</u> CG <u>CG</u> <u>CT</u> CT <u>CC</u> ACAT <u>CA</u> AT <u>CC</u> TT <u>AC</u> AC <u>GG</u>	5753
	CGTAGTAAGGATTGATGTGGAGAGCCGC <u>GT</u> GC <u>AT</u> AC <u>CT</u> AC <u>AG</u> AAT <u>CC</u> CTG <u>CT</u> CAG <u>TT</u> <u>GT</u> <u>GA</u> AT <u>AG</u> C <u>CT</u> CC <u>CT</u> G <u>TT</u> G <u>AG</u> <u>TT</u> <u>AC</u> CTGTGTTGCCGACC <u>AC</u> <u>TT</u> AA <u>TT</u> AG <u>GT</u> <u>GC</u>	5754
	CTATT <u>CA</u> CA <u>CT</u> <u>GA</u> <u>G</u>	5755
	CTCAG <u>TT</u> <u>GT</u> <u>GA</u> ATA <u>GA</u>	5756
25 Lys Overproduction DHPS 1 <i>Triticum aestivum</i>	TCAT <u>CG</u> GG <u>CA</u> ACT <u>GT</u> <u>TA</u> CT <u>GC</u> <u>TT</u> <u>GG</u> <u>AG</u> <u>CC</u> <u>AA</u> <u>CT</u> <u>AA</u> <u>AG</u> <u>GT</u> <u>AT</u> AGG <u>CA</u> AC <u>AC</u> <u>GG</u> <u>AA</u> <u>A</u> TA <u>CT</u> <u>CA</u> <u>AC</u> <u>CC</u> <u>AG</u> <u>AG</u> <u>GA</u> <u>AG</u> <u>GT</u> <u>TT</u> <u>CA</u> <u>CG</u> <u>GA</u> CAG <u>AG</u> <u>CG</u> <u>GG</u> <u>AT</u> <u>TT</u> <u>GT</u> <u>GG</u> <u>C</u> <u>AT</u> <u>GC</u> <u>GC</u>	5757
Ser165Asn AGT-AAT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCATGCATGCCAACAGCAAATCCCTGCTCTGCGGTGAACAGCT TCTCTGGTTGAGTTA <u>TT</u> CCCGTGTGCCTATCACTTAATGTTGG CTCCAAAGCAGTTAACAGTATGCCGATGA	5758
	CACGGGAA <u>A</u> TAACCTCAA	5759
	TTGAGTTA <u>T</u> CCCGTG	5760
5 Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Val GCG-GTG	GAGCCAACATTAAAGTGTAGGCAACACGGGAAGTAACCTAACCA GAGAAGCTGTTCAC <u>G</u> TCAGACAGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTTCATGTCAATCCTACTACGG	5761
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGT <u>C</u> ACGTGAACAGCTCTCTGGTTGAGTTACTT CCCGTGTGCCTATCACTTAATGTTGGCTC	5762
	TGTTCAC <u>G</u> TGACAGAGC	5763
	GCTCTGT <u>C</u> ACGTGAACA	5764
	GGAGCCAACATTAAAGTGTAGGCAACACGGGAAGTAACCTAACCC AGAGAAGCTGTTCAC <u>G</u> ACAGACAGAGCAGGGATTGCTGTTGGCAT GCATGCAGCTCTTCATGTCAATCCTACTACGG	5765
10 Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Thr GCG-ACG	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGT <u>C</u> GTGAACAGCTCTCTGGTTGAGTTACTTC CCGTGTGCCTATCACTTAATGTTGGCTC	5766
	CTGTTCAC <u>G</u> ACAGAG	5767
	CTCTGT <u>C</u> GTGAACAG	5768
	TCATGGGCACACTGTAACTGCTTGGAACTAACATTAAAGTGT AGGCAACACGGGA <u>A</u> TAACCTCAACTAGAGAACGATTACGCTTC AGAGCAGGGATTGCTGTTGGCATGCATGC	5769
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT TCTCTAGTTGAGTTA <u>T</u> CCCGTGTGCCTATCACTTAATGTTAGT TCCAAAGCAGTTAACAGTGTGCCGATGA	5770
15 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ser154Asn AGT-AAT	CACGGGAA <u>A</u> TAACCTCAA	5771
	TTGAGTTA <u>T</u> CCCGTG	5772
	GAACTAACATTAAAGTGTAGGCAACACGGGAAGTAACCTAACCA GAGAAGCGATT <u>C</u> ACG <u>T</u> TCAGAGCAGGGATTGCTGTTGGCATGC ATGCAGCTCTCCATGTCAATCCTACTATGG	5773
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAA <u>AC</u> GTGAATCGCTCTAGTTGAGTTACTTC CCGTGTGCCTATCACTTAATGTTAGTTC	5774
	GATTCA <u>C</u> GT <u>T</u> TCAGAGC	5775
20 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Val GCT-GTT	GCTCTGAA <u>AC</u> GTGAATC	5776

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Thr GCT-ACT	GGAACTAACATTAAAGTGTAGGCAACACGGGAAGTAACACTCACT AGAGAAGCGATTCAC <u>A</u> CTTCAGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTCCATGTCAATCCTTACTATG	5777
		CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA ATCCCCTGCTCTGAAG <u>I</u> GTGAATCGCTCTAGTTGAGTTACTTCC CGTGTGCCTATCACTTTAATGTTAGTTCC	5778
		CGATTCA <u>C</u> ACTTCAGAG	5779
		CTCTGAAG <u>I</u> GTGAATCG	5780
10	Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ser154Asn AGT-AAT	CTCAATTGGGCATACTGTGA <u>A</u> CTGCTTGGCTCTAGAATTAAAGTGA TAGGCAACACAGGAA <u>A</u> TA <u>A</u> CTCAACCAGAGAAGCTGTTACGC CAGAGCAGGGATTGCTGTTGGCATGCATG	5781
		CATGCATGCCAACAGCAA <u>A</u> TCCTGCTCTGTTGCGTAACAGCTT CTCTGGTTGAGTT <u>A</u> TTCCCTGTGTTGCCTATCACTTTAATTCTAGA GCCAAAGCAGTTCACAGTATGCCCAATGAG	5782
		CACAGGAA <u>A</u> TA <u>A</u> CTCAA	5783
		TTGAGTT <u>A</u> TTCCCTGTG	5784
15	Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Val GCA-GTA	GCTCTAGAATTAAAGTGTAGGCAACACAGGAAGTAACCAACCA GAGAAGCTGTT <u>C</u> ACG <u>T</u> ACAGAGCAGGGATTGCTGTTGGCATGC ATGCAGCTCTCCACATCAATCCTTACTATGG	5785
		CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA AATCCCCTGCTCTGTT <u>A</u> CGTGAACAGCTCTGGTTGAGTTACTTC CTGTGTTGCCTATCACTTTAATTCTAGAGC	5786
		TGTTCAC <u>G</u> TAACAGAGC	5787
		GCTCTGTT <u>A</u> CGTGAACA	5788
20	Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Thr GCA-ACA	GGCTCTAGAATTAAAGTGTAGGCAACACAGGAAGTAACCAACCA AGAGAAGCTGTT <u>C</u> AC <u>A</u> CAACAGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTCCACATCAATCCTTACTATG	5789
		CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA ATCCCCTGCTCTGTT <u>I</u> GTGAACAGCTCTGGTTGAGTTACTTC TGTGTTGCCTATCACTTTAATTCTAGAGCC	5790
		CTGTTCAC <u>A</u> CAACAGAG	5791
		CTCTGTT <u>I</u> GTGAACAG	5792
25	Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ser136Asn AGC-AAC	TCATTGGTCACACAGTCATTGTTGGAGGGCCATCAAAGTCAT CGGGAACACTGGAA <u>A</u> CA <u>T</u> CCACAAGGGAAAGCAATCCATGCAA CTGAACAGGGATTGCTGTAGGTATGCATGC	5793
		GCATGCATACCTACAGCAA <u>A</u> CCCTGTT <u>C</u> AGTTGCATGGATTGCTT CCCTTGAGTT <u>I</u> GTGAACAGCTCTGGTTGACTTTGATGGACC CTCCAAAACAATTGACTGTGTGACCAATGA	5794
		CACTGGAA <u>A</u> CAACTCCA	5795

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		TGGAGTTG T CCAGTG	5796
5	Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGGAACACTTGGAAAGCAACTCCACAA GGGAAGCAATCCATGT A ACTGAACAGGGATTGCTGTAGGTATGC ATGCAGCTTCACATTAATCCCTACTATGG	5797
		CCATAGTAGGGATTAAATGTGAAGAGCTGCATGCATAACCTACAGCA AATCCCTGTT C AGTT A ATGGATTGCTTCCCTGTGGAGTTGCTTC CAGTGTCCC G ATGACTTTGATGGACCCTC	5798
		AATCCATGT A ACTGAAC	5799
		GTTCAGTT A ATGGATT	5800
10	Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Thr GCA-ACA	GGAGGGTCCATCAAAGTCATCGGGAACACTTGGAAAGCAACTCCAC AAGGGAAAGCAATCCAT A CAACTGAACAGGGATTGCTGTAGGTAT GCATGCAGCTTCACATTAATCCCTACTATG	5801
		CATAGTAGGGATTAAATGTGAAGAGCTGCATGCATAACCTACAGCAA ATCCCTGTT C AGTT G ATGGATTGCTTCCCTGTGGAGTTGCTTC AGTGTCCC G ATGACTTTGATGGACCCTC	5802
		CAATCCAT A CAACTGAA	5803
		TTCAGTTG T ATGGATTG	5804
		TTATAGGCCATACCG T AACTG T GGCGGAAGCATCAAAGTCAT TGGAAACACTGGAAA A CAATTGACTAGAGAAGCAATCCACCGCGAC TGAACAAGGATTGCCGGTTGGATGCATGC	5805
15	Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ser142Asn AGC-AAC	GCATGCATTCCAACCGCGAATCCTGTT C AGTCGCGTGGATTGCT TCTCTAGTCGAATTG T CCAGTGT T CCAATGACTTTGATGCTTC CGCCAAAACAGTTAACGGTATGGCCTATAA	5806
		CACTGGAAA A CAATTGCA	5807
		TCGAATTG T CCAGTG	5808
		GGCGGAAGCATCAAAGTCATTGGAAACACTTGGAAAGCAATTGACTA GAGAAGCAATCCACGT G ACTGAACAAGGATTGCCGGTTGGATGC	5809
20	Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Val GCG-GTG	ATGCTGCTTCATATAAACCC T ACTATGG	5810
		CCATAGTAAGGGTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCC T GTT C AGTC A GTGGATTGCTTCTAGTCGAATTGCTTC CAGTGT T CCAATGACTTTGATGCTTC	5811
		AATCCACGT G ACTGAAC	5812
		GTTCAGTC A GTGGATT	
25	Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Thr GCG-ACG	GGCGGAAGCATCAAAGTCATTGGAAACACTTGGAAAGCAATTGACT AGAGAAGCAATCCAC A CGACTGAACAAGGATTGCCGGTTGGATGC	5813
		CATGCTGCTTCATATAAACCC T ACTATG CATAGTAAGGGTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCC T GTT C AGTC G GTGGATTGCTTCTAGTCGAATTGCTTC AGTGT T CCAATGACTTTGATGCTTC	5814

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		CAATCCACACGACTGAA	5815
		TTCAGTCGTGTGGATTG	5816
5	Lys Overproduction DHPS <i>Glycine max</i> Ser103Asn AGC-AAC	TTATTGCTCATACAGTCAACTGTTGGTGGGAAAATAAGGTATT GGAAATACTGGAA <u>A</u> CAACTCCACCAGGGAGCAATTATGCCACT GAGCAGGGTTTGCTGTTGGAATGCATGC	5817
		GCATGCATCCAACAGCAA <u>A</u> CCCTGCTCAGTGGCATGAATTGCT TCCCTGGAGTTG <u>T</u> TCAGTATTCCAATAACCTTAATTTC CACCAAAACAGTTGACTGTATGAGCAATA	5818
		TACTGGAA <u>A</u> CAACTCCA	5819
		TGGAGTTG <u>T</u> TCAGTA	5820
		GTGGGAAAATAAGGTTATTGGAATACTGGAAGCAACTCCACCA GGGAAGCAATTATG <u>T</u> CACTGAGCAGGGTTTGCTGTTGGAATGC	5821
10	Lys Overproduction DHPS <i>Glycine max</i> Ala112Val GCC-GTC	ATGCTGCCCTTCACATAACCTTACTATGG	
		CCATAGTAAGGGTTATGTGAAGGGCAGCATGCATTCAAACAGCA AAACCTGCTCAGTG <u>A</u> CATGAATTGCTTCCCTGGTGGAGTTGCTT CCAGTATTCCAATAACCTTAATTCCCAC	5822
		AATTATG <u>T</u> CACTGAGC	5823
		GCTCAGTG <u>A</u> CATGAATT	5824
		GGTGGGAAAATAAGGTTATTGGAATACTGGAAGCAACTCCACCA AGGGAA <u>G</u> CAATT <u>T</u> ACCACTGAGCAGGGTTTGCTGTTGGAATG	5825
15	Lys Overproduction DHPS <i>Glycine max</i> Ala112Thr GCC-ACC	CATGCTGCCCTTCACATAACCTTACTATG	
		CATAGTAAGGGTTATGTGAAGGGCAGCATGCATTCAAACAGCAA AAACCTGCTCAGTG <u>T</u> ATGAATTGCTTCCCTGGTGGAGTTGCTTC CAGTATTCCAATAACCTTAATTCCCAC	5826
		CAATT <u>C</u> AT <u>A</u> CCACTGAG	5827
		CTCAGTGG <u>T</u> ATGAATTG	5828
		CTTGCAGGAGACATATT <u>C</u> AGATCGTGCTGAGTCACGTTTGAG CGGCGAACATTG <u>C</u> AA <u>A</u> CCCTTGAAGTTATAGAGCACTAAGA	5829
20	Trp Overproduction AS <i>Arabidopsis thaliana</i> Asp341Asn GAC-AAC	GTTGTGAATCCAAGTCCGTATATGGTTATT	
		AATAACCCATATACGGACTTGGATT <u>C</u> ACA <u>A</u> CTCTAGTGCTCTATA AACTCAAAGGGGT <u>T</u> GC <u>A</u> ATGTTCGCCGCTCAAACGTTGACT	5830
		CAGCACGATCTGA <u>A</u> ATATG <u>T</u> CTCCTGCAAG	
		CATT <u>T</u> G <u>C</u> AA <u>A</u> CCCTT	5831
		AAAGGGGT <u>T</u> GC <u>A</u> ATG	5832
25	Trp Overproduction AS <i>Nicotiana tabacum</i>	GCTGCAGGAGACATATT <u>C</u> AA <u>A</u> CT <u>C</u> GTTTAAGTCACGCTTGAGA GAAGAACATTG <u>C</u> TA <u>A</u> CCATTGAAGTGACAGAGCATTAAAGAAT	5833
		TGTGAATCCAAGCCATATATGACTTACA Asp326Asn GAC-AAC	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Trp Overproduction AS <i>Oryza sativa</i> Asp323Asn GAC-AAC	TGTAAGTCATATATGGGCTGGATTACAATTCTTAATGCTCTGTA CACTTCAAATGGGT I AGCAAATGTTCTCTCAAAGCGTTGACTT AAAACGATTGAAATATGTCTCCTGCAGC	5834
		CATTTGCT A ACCCATT	5835
		AAATGGGT T AGCAAATG	5836
10	Trp Overproduction AS <i>Ruta graveolens</i> Asp354Asn GAC-AAC	CTAGCTGGTGACATTTCAAGTAGTCTTAAGCCAGCGTTTGAGA GGCGTACATTGCT A ACCCCTTGAGGTGACCGTGCAATTGCGTA TTGTCATCCTAGTCCTTATATGGCCTATC	5837
		GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAGGGGT T AGCAAATGTACGCCCTCAAAACGCTGGC TTAAGACTACTTGA AAA ATGTCAACCAGCTAG	5838
		CATTTGCT A ACCCCTT	5839
		AAAGGGGT T AGCAAATG	5840
		CTTGCTGGTGACATATCCAGATCGTACTAAGTCAGCGTTTGAAA GGCGAACGTTCGCA A ACCCATTGAAATCTATAGATCACTGAGGA TTGTTAATCCAAGCCC A TATATGACTTATT	5841
15	Trp Overproduction AS <i>Catharanthus roseus</i> Asp354Asn GAT-AAT	AATAAGTCATATATGGGCTGGATTACAATCCTCAGTGATCTATA GATTCAAATGGGT T TGCGAACGTTGCCCTCAAAACGCTGACTT AGTACGATCTGGAATATGTCAACCAGCAAG	5842
		CGTCGCA A ACCCATT	5843
		AAATGGGT T TGCGAACG	5844
		CTGGCTGGGGACATATTCCAGCTTGTCTAAGTCAGCGTTTGAA CGGCGAACATTGCA A ATCCATTGAAGTCTACCGAGCATTGAGA ATTGTCAACCC A AGTCC A TATATGACTTATT	5845
		AATAAGTCATATATGGACTTGGGTGACAATTCTCAATGCTCGGTA GACTTCAAATGGAT T TGCAAATGTTGCCGTTCAAACGCTGACTT AGGACAAGCTGGAATATGTCCCCAGCCAG	5846
		CATTTGCA A ATCCATT	5847
		AAATGGATTGCAAATG	5848

Example 10**Production of modified starch in plants**

A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of α -1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional α -1,6-glycosidic linkages. In plants from which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunken* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 20
Genome-Altering Oligos Conferring Increased Starch

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Ala99Lys GCA-AAA	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGAGGTGGAA <u>AAAGGA</u> ACTCGACTCTTCCTCTCACAAA CGCCGCGCCAAGCCTGCCGTTCTATCGGGG	5849
		CCCCGATAGGAACGGCAGGCTGGCGCGCGTTTGAGAGGA AAGAGTCGAGTTCTTCCACCTCCAAGAATAATGGAAGCAACT GTCCTGGATCCCTTCTCAGTCTCAAGTTC	5850
		GAGGTGG <u>AAAGGA</u> ACT	5851
		AGTTCC <u>TTT</u> CCACCTC	5852
10	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro127Leu CCA-CTA	CAAAACGCCGCCAAGCCTGCCGTTCTATCGGGGGAGCCTAT AGG <u>TG</u> ATAGATGTACT <u>AAT</u> GAGCAATTGTATTAACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC	5853
		GAGTTATATTGTGTAGTATGTAGACTTTGTTGATTCCGCTGTTAA TACAATTGCTCATT <u>AG</u> TACATCTATCAACCTATAGGCTCCCCGAT AGGAACGGCAGGCTGGCGCGCGTTTG	5854
		AGATGT <u>ACT</u> <u>AAT</u> GAGCA	5855
		TGCTCATT <u>AG</u> TACATCT	5856
		TCACACAA <u>TATA</u> ACTCAGCATCATTGAACAGGCATTAGCCCGTGC TTACA <u>ACTCCA</u> AT <u>AA</u> CTTGCTTGGAGATGGCTATGTTGAGGTT CTTGC <u>GGCC</u> ACTCAA <u>ACGCC</u> AGGAGAACATC	5857
15	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT	GATTCTCCTGGCGTTGAGTGGCCGCAAGAACCTAACATAGCCA TCTCAAAGCCAAG <u>ATT</u> ATTGGAGTTGTAAGCACGGCTAAATGC CTGTTCAATGATGCTGAGTTATTTGTGTGA	5858
		CTCCA <u>AT</u> <u>AA</u> CTTGCT	5859
		AGCCAAG <u>ATT</u> ATTGGAG	5860
		TCACACAA <u>TATA</u> ACTCAGCATCATTGAACAGGCATTAGCCCGTGC TTACA <u>ACTCCA</u> AT <u>AA</u> CTTGCTTGGAGATGGCTATGTTGAGGTT CTTGC <u>GGCC</u> ACTCAA <u>ACGCC</u> AGGAGAACATC	5861
		GATTCTCCTGGCGTTGAGTGGCCGCAAGAACCTAACATAGCCA TCTCAAAGCCAAG <u>GG</u> TTATTGGAGTTGTAAGCACGGCTAAATGC CTGTTCAATGATGCTGAGTTATTTGTGTGA	5862
20	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT	CTCCA <u>AT</u> <u>AA</u> CTTGCT	5863
		AGCCAAG <u>GG</u> TTATTGGAG	5864
25	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAC	TCACACAA <u>TATA</u> ACTCAGCATCATTGAACAGGCATTAGCCCGTGC TTACA <u>ACTCCA</u> AT <u>AA</u> CTTGCTTGGAGATGGCTATGTTGAGGTT CTTGC <u>GGCC</u> ACTCAA <u>ACGCC</u> AGGAGAACATC	5861
		GATTCTCCTGGCGTTGAGTGGCCGCAAGAACCTAACATAGCCA TCTCAAAGCCAAG <u>GG</u> TTATTGGAGTTGTAAGCACGGCTAAATGC CTGTTCAATGATGCTGAGTTATTTGTGTGA	5862

	Phenotype Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Asn100Lys AAT-AAA	GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT TCTAGGAGGAGGCC <u>A</u> GGAGCTAACTCTCCCTCTTACAATGAG AGCCGCACACACCAGCTGAAATATTCACTT	5865
		AAGATGAATATTACAGCTGGTGTGGCCTCTCATTGTAAGAGG GAAGAGTTAGCTCC <u>T</u> GCCTCCTCTAGAATGATTGCAGCCAC ATTTGCGGGTCTACCTTCTCTCTCAAAC	5866
		GGAGGCC <u>A</u> GGAGCTAA	5867
		TTAGCTCC <u>T</u> GCCTCC	5868
10	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro128Leu CCG-CTG	CTTGTGTCTCAAATTATGTTAGGTCCTGTTGGATGCTACAG GCTGATCGATATCCT <u>I</u> GATGAGTAACGTATTAAACAGCTGCATCAAC AAGATATTGTGCTGACACAGCTCAACTC	5869
		GAGTTGAACTGTGTCAGCACAAATATCTTGTGATGCAGCTGTTAA TACAGTTACTCAT <u>C</u> AGGATATCGATCAGCCTGTAGCATCCACCAA CAGGAACCTAACATAATTGAAAGACACAAG	5870
		CGATATCC <u>I</u> GATGAGTA	5871
		TACTCAT <u>C</u> AGGATATCG	5872
		TGACACAGTCAACTCAGCTCCCTAACATCGACATTAGCACCGAAC TTATTTGGA <u>A</u> TA <u>A</u> TAAACTTGGAGGTGGTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5873
15	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAT	GCTGAGAGTTATTATTGTATAGTGTGTTGACCTCTACGAAACCAC CTCCAAAGTTAT <u>A</u> TT <u>A</u> TTCCAAAATAAGTTCGTGTAAATGTCG ATTAAGGGAAGCTGAGTTGAACGTGTCA	5874
		TGGGA <u>A</u> TA <u>A</u> TAAACT	5875
		AGTTTAT <u>A</u> TT <u>A</u> TTCCCA	5876
		TGACACAGTCAACTCAGCTCCCTAACATCGACATTAGCACCGAAC TTATTTGGA <u>A</u> ACATAAAACTTGGAGGTGGTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5877
20	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAC	GCTGAGAGTTATTATTGTATAGTGTGTTGACCTCTACGAAACCAC CTCCAAAGTTAT <u>G</u> TTATTCCAAAATAAGTTCGTGTAAATGTCG ATTAAGGGAAGCTGAGTTGAACGTGTCA	5878
		TGGGA <u>A</u> TA <u>A</u> CATAAACT	5879
		AGTTTAT <u>G</u> TTATTCCCA	5880
		TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCCTGTCA TTCTAGGTGGTGG <u>A</u> AGGAACTCGTCTTCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCTTATTGGTGG	5881
25	Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Val94Lys GTT-AAA	CCACCAATAGGAACAGCTGGTTAGCTCTGCTTGAAGAGGA AAAAGACGAGTT <u>C</u> TTACCACCACTAGAATGACAGAGGCAACA GCTTTGGATCTGCCGTTGGTTCTCAA	5882
		TGGTGG <u>A</u> AGGAACTC	5883

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		GAGTCCTTACCA	5884
5	Increased Starch ADPGPP <i>Lycopersicon</i> <i>esculentum</i> Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAACCGCTTCCATTGGTGGTTACCGTA GGCTAATTGATGTACAAATGAGTAAC TGCACTAACAGTGGCATAC GGAAAATTTCATCTAACACAGTTCAATT	5885
		GAATTGAAC TGTGTTAAGATGAAAATTTCGTATGCCACTGTTAA TGCAGTTACTCATTGTACATCAATTAGCCGGTAACAACCACCAAT AGGAACAGCTGGTTAGCTCTTGCTTG	5886
		TGATGTACAAATGAGTA	5887
		TACTCATTGTACATCA	5888
10	Increased Starch ADPGPP <i>Lycopersicon</i> <i>esculentum</i> Gly158Asn GGA-AAT	CACAGTTCAATTCCCTTCCCTCAATCGTCACCTGCCGCACGTA TAATTTGAAATAATGTGGTTGGAGATGGATTGTGGAGGTT TTAGCTGCAACCCAGACTCCAGGGGATGC	5889
		GCATCCCCGGAGTCTGGGTTGCAGCTAAACCTCCACAAATCCA TCTCCAAAACCCACATTATTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAAGTGT	5890
		TGGAAATAATGTGGTT	5891
		AACCCACATTATTCCA	5892
15	Increased Starch ADPGPP <i>Lycopersicon</i> <i>esculentum</i> Gly158Asn GGA-AAC	CACAGTTCAATTCCCTTCCCTCAATCGTCACCTGCCGCACGTA TAATTTGAAATAACGTGGTTGGAGATGGATTGTGGAGGTT TTAGCTGCAACCCAGACTCCAGGGGATGC	5893
		GCATCCCCGGAGTCTGGGTTGCAGCTAAACCTCCACAAATCCA TCTCCAAAACCCACGTTATTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAAGTGT	5894
		TGGAAATAACGTGGTT	5895
		AACCCACGTTATTCCA	5896
20	Increased Starch ADPGPP <i>Cicer arietinum</i> Ala101Lys GCT-AAA	ACGTAGATTGGAAAAAGAGACCAAGTACAGTTGTAGCAATTAT ACTAGGTGGAGGTAAAGGAAC TCGTCTTCCCTCTCACCAAGC GACGAGCCAAGCCTGCTTCCAATTGGAGG	5897
		CCTCCAATTGGAACACAGCAGGCTTGGCTCGTCGCTGGTGAGAGG GAAGAGACGAGTCTTACCTCACCTAGTATAATTGCTACA GTACTTGGGTCTCTTCCAAATCTACGT	5898
		TGGAGGTAAAGGAACCT	5899
		GAGTCCTTACCTCCA	5900

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased Starch ADPGPP <i>Cicer arietinum</i> Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA GGCTGATAGATGTACTAATGAGTAAC TGCA TCA ATAGTGGGATCAA CAAAGTATACTACATTCTCACTCAATTTAACCTTAA	5901
		GAATTAATTGAGTGAGAATGTACTTGTGATCCCACATTGAT GCAGTTACTCATTAGTACATCTATCAGCCTATAAGCACCTCCAATT GGAACAGCAGGCTTGGCTCGTCGCTTGG	5902
		AGATGTACTAATGAGTA	5903
		TACTCATTAGTACATCT	5904
10	Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAT	CTCAATTAAATT CAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAAC TCTGGTACTAATGTCAC TTTGGAGATGGCTATGTTGAGGTT CTTGCAGCACTCAA ACTCCAGGGGAGCA	5905
		TGCTCCCTGGAGTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACATTAGTACCA GAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	5906
		TGGTACTAATGTCAC TT	5907
		AAGTGACATTAGTACCA	5908
15	Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAC	CTCAATTAAATT CAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAAC TCTGGTACTAACGTCACTTTGGAGATGGCTATGTTGAGGTT CTTGCAGCACTCAA ACTCCAGGGGAGCA	5909
		TGCTCCCTGGAGTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACGTTAGTACCA GAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	5910
		TGGTACTAACGTCACTT	5911
		AAGTGACGTTAGTACCA	5912
20	Increased Starch ADPGPP <i>Ipomoea batatas</i> Ala94Lys GCA-AAA	ATATTGGAGAGGCCGTGGGCAAACCCCTAAGAATGTGGCTGCAATC ATACTGCCAGGCCGTAAAGGGACACACCTATTCCCTCTCACCAAT CGAGCTGCAACCCCTGCTGTTCCACTTGGAG	5913
		CTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGGTAGAGGG AATAGGTGTGTCCTTTACCGCCTGGCAGTATGATTGAGCCACA TTCTTAGGGTTGCCGACGCCCTCCAATAT	5914
		CAGGCCGTAAAGGGACA	5915
		TGTCCCTTACCGCCTG	5916
25	Increased Starch ADPGPP <i>Ipomoea batatas</i> Pro122Leu CCA-CTA	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGTGCTATA GGTTGATCGACATTCTAATGAGCAACTGCATCAACAGCGGGGTTA ACAAGATCTTGTGCTGACCCAGTTCAATTC	5917
		GAATTGAAC TGGGT CAGCACA AAGATCTGTTAACCCGCTGTTG ATGCAGTTGCTCATTAGAATGTGATCAACCTATAGCATCCTCAA GTGGAACAGCAGGGGTTGCAGCTGATTGG	5918
		CGACATTCTAATGAGCA	5919

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		TGCTCATTAGAATGTCG	5920
5	Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAT	TGACCCAGTTCAATTAGCTTCTTAACCGTCACATTCCCGTAC CGTCTTGGA <u>A</u> ATGTGAGCTTCGGAGATGGATTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5921
		GTTCCTTGTGTTGGGTTGCCAGCCAGCACCTAACAAATCCA TCTCCGAAGCTCAC <u>A</u> TTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGA <u>ACTGGGTCA</u>	5922
		TGGCA <u>A</u> ATGTGAGCT	5923
		AGCTCAC <u>A</u> TTGCCA	5924
10	Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAC	TGACCCAGTTCAATTAGCTTCTTAACCGTCACATTCCCGTAC CGTCTTGGA <u>A</u> ACGTGAGCTTCGGAGATGGATTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5925
		GTTCCTTGTGTTGGGTTGCCAGCCAGCACCTAACAAATCCA TCTCCGAAGCTCAC <u>G</u> TTATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGA <u>ACTGGGTCA</u>	5926
		TGGCA <u>A</u> ACGTGAGCT	5927
		AGCTCAC <u>G</u> TTATTGCCA	5928
15	Increased Starch ADPGPP <i>Oryza sativa</i> Thr96Lys ACC-AAA	CATTCCGGAGGA <u>A</u> CTTGCGGATCCAAATGAGGTTGCTGCTGTTA TATTGGGTGGTGG <u>C</u> AA <u>AGGG</u> ACTCAACTTTCTCCTCACAGCA CAAGGGCCACGCC <u>TG</u> CTGTTCTATTGGAGG	5929
		CCTCCAATAGGAACAGCAGGCGTGGCC <u>TG</u> GCTTGAGAGG AAAAAGTTGAGT <u>CC</u> CTTGCCACCACCCAA <u>TATAAC</u> AGCAGCAAC CTCATTGATCCGCAA <u>AG</u> TTCTCCCGGAATG	5930
		TGGTGG <u>C</u> AA <u>AGGG</u> ACTC	5931
		GAGTCC <u>C</u> TTGCCACCA	5932
20	Increased Starch ADPGPP <i>Oryza sativa</i> Pro124Leu CCC-CTC	CAAGCACA <u>AGGG</u> CCACGCC <u>TG</u> CTGTTCTATTGGAGGATGCTATA GGCTTATCGATATCC <u>C</u> ATGAGCA <u>CT</u> GGTCAACAGTGGCATAAA CAAGATATT <u>C</u> ATA <u>ATG</u> ACTCAATT <u>C</u> ACTC	5933
		GAGTTGAATTGAGTCATTATGAATATCTTGTTATGCCACTGTTGAA ACAGTTGCTCAT <u>G</u> AGGATATCGATAAGCCTATAGCATCCTCCAATA GGAACAGCAGGCGTGGCC <u>TG</u> GCTTG	5934
		CGATAT <u>C</u> CTCATGAGCA	5935
		TGCTCAT <u>G</u> AGGATATCG	5936
25	Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAT	TGACTCAATTCAACTCAGCATCTTAATCGTCACATT <u>C</u> ATCGTAC GTACCTGGTGG <u>A</u> ATCAACTTACTGATGGTT <u>C</u> TGTTGAGGTA TTAGCCGCTACACAA <u>ATGC</u> CTGGGGAGGC	5937
		GCCTCCCCAGGC <u>A</u> TTGTGAGCGGCTAACACCTAACAGAACCA TCAGTAAAGTTGAT <u>A</u> TTACCACCAAGGTACGTACGATGA <u>ATGTGAC</u> GATTAAGAGATGCTGAGTTGAATTGAGTC	5938

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGTGGTAATATCAACT	5939
	AGTTGATATTACCACCA	5940
5 Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCACTCGTAC GTACCTTGGTGGTAACATCAACTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAATGCCTGGGGAGGC	5941
	GCCTCCCCAGGCATTGTGAGCGGCTAATACCTAACAGAACCA TCAGTAAAGTTGATGTTACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	5942
	TGGTGGTAACATCAACT	5943
	AGTTGATGTTACCACCA	5944
10 Increased Starch ADPGPP <i>Triticum aestivum</i> Thr80Lys ACC-AAA	GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGCGGCAAAGGGACTCAGCTTCCCACTCACGAG CACAGGGCCACACCTGCTGTTCTATTGGAGG	5945
	CCTCCAATAGGAACACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCCATTGCCGCCGCCAGTATGACGGCCGCAA CCTCGTTGGATCGCTTAATCCTCTGAAGGAC	5946
	CGGCAGGCAAAGGGACTC	5947
	GAGTCCCATTGCCGCCG	5948
15 Increased Starch ADPGPP <i>Triticum aestivum</i> Pro108Leu CCC-CTC	CGAGCACAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGACATTCTCATGAGCACTGCTCAACAGTGGCATCA ACAAGATATTGTCATGACCCAGTTCAACTC	5949
	GAGTTGAACTGGGTATGACGAATATCTGTTGATGCCACTGTTG AAGCAGTTGCTCATGAGAATGTCGATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	5950
	CGACATTCTCATGAGCA	5951
	TGCTCATGAGAATGTCG	5952
20 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTACCGCA CCTACCTCGCGGGAAATATCAATTCACTGATGGATCCGTTGAGG TATTGGCCCGACGCAAATGCCGGGGAGGC	5953
	GCCTCCCCGGCATTGCGTCGCGGCCAATACCTAACGGATCC ATCACTGAAATTGATATTCCGCCAGGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGGAGCTGAGTTGAACTGGTCA	5954
	CGGCAGGAAATATCAATT	5955
	AATTGATAATTCCGCCG	5956
25 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTACCGCA CCTACCTCGCGGGAAACATCAATTCACTGATGGATCCGTTGAGG TATTGGCCCGACGCAAATGCCGGGGAGGC	5957

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5		GCCTCCCCGGGCATTGCGTCGCCAACACCTAACGGATCC ATCAGTGAAATTGAT <u>GTT</u> CCCCGGAGGTAGGTGCCGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACGGTCA	5958
		CGGCGGG <u>AAC</u> ATCAATT	5959
		AATTGAT <u>GTT</u> CCCAGCG	5960
10	Increased Starch ADPGPP <i>Oryza sativa</i> Thr95Lys ACT-AAA	CCTCCCAGAAAGAATTATGCTGATGCAAGGCCACGTTCTGCTGTCA TTTGGGGGGAGGCAA <u>AGGAG</u> TTCAACTCTTCCTGTGACAAGCA CAAGGGCTACCCCCGCTGTTCTGTGGAGG	5961
		CCTCCAACAGGAACAGCGGGGGTAGCCCTTGTGCTTGTCAAGGG AAAGAGTTGAACCT <u>CC</u> TGCCTCCACCCAAAATGACAGCAGAAC GTGGCTTGATCAGCATAATTCTTCGGGAGG	5962
		TGGAGG <u>CAAAGGAG</u> TTC	5963
		GAAC <u>ACTCC</u> TGCCTCCA	5964
		CAAGCACAAGGGCTACCCCCGCTGTTCTGTGGAGGATGTTACA GGCTTATTGACAT <u>CC</u> TATGAGCAATTGCTCAATAGCGGAATAAA TAAAATATTGTGATGACTCAG <u>TT</u> CAATT	5965
15	Increased Starch ADPGPP <i>Oryza sativa</i> Pro123Leu CCT-CTT	GAATTGAAC <u>TGAGT</u> CATCACAAATATT <u>TT</u> ATTCCGCTATTGAA GCAATTGCTCATA <u>AGGAT</u> GTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTGTGCTTG	5966
		TGACAT <u>CC</u> TATGAGCA	5967
		TGCTCATA <u>AGGAT</u> GTCA	5968
		TGACTCAG <u>TT</u> CAATTCTGCTTCTTAATGCCATATCCATCATAC ATAC <u>CTTGGTGGGAA</u> ATCAACTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5969
		GGTCGTCAGGCATTG <u>TGAGC</u> AGCCAATACCTGCACAGACCCA TCAGTAAAG <u>TTGAT</u> TTCCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAA <u>TTGAA</u> CTGAGTCA	5970
20	Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAT	TGGTGG <u>GAAT</u> CAACT AGTTGAT <u>TTCCCACCA</u>	5971 5972
		TGACTCAG <u>TT</u> CAATTCTGCTTCTTAATGCCATATCCATCATAC ATAC <u>CTTGGTGGGAA</u> ACATCAACTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5973
		GGTCGTCAGGCATTG <u>TGAGC</u> AGCCAATACCTGCACAGACCCA TCAGTAAAG <u>TTGAT</u> TTCCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAA <u>TTGAA</u> CTGAGTCA	5974
		TGGTGG <u>GAAC</u> ATCAACT	5975
		AGTTGAT <u>TTCCCACCA</u>	5976

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased Starch ADPGPP <i>Triticum aestivum</i> Thr99Lys ACC-AAA	CCTTCCGCAGGAATTACGCCGATCGAACGAGGTCGGCGCGTC ATACTCGGCGGTGGCA <u>AAGG</u> GACTCAGCTTCCCTCTCACAG CACAAGGCCACACCTGCTGTTCTATTGGAGG	5977
		CCTCCAATAGGAACACAGCAGGTGTGGCCCTTGCTTGAGAGG GAAGAGCTGAGTCCC <u>TT</u> GCCACCGCCGAGTATGACGGCCGCA CCTCGTTCGGATCGCGTAATTCCCTGCGGAAGG	5978
		CGGTGGCA <u>AAGG</u> ACTC	5979
		GAGTCCC <u>TT</u> GCCACCG	5980
10	Increased Starch ADPGPP <i>Triticum aestivum</i> Pro127Leu CCC-CTC	CAAGCACAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGATATT <u>C</u> CATGAGCACTGCTCAATAGTGGCATCAA CAAGATATT <u>C</u> GTATGACGCA <u>GT</u> TCAC	5981
		GAGTTGA <u>ACT</u> CGTCATGACGA <u>AT</u> ATCTGTTGATGCCACTATTGA AGCAGTTGCTCAT <u>G</u> AGA <u>AT</u> ATCGATGAGCCTGTAACATCCTCAA TAGGAACACAGCAGGTGTGGCCCTTGCTTG	5982
		CGATATT <u>C</u> CATGAGCA	5983
		TGCTCAT <u>G</u> AGA <u>AT</u> ATCG	5984
		TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTACCGCA CCTACCTCGGCGGG <u>A</u> ATCAATT <u>C</u> ACTGATGGATCTGTTGAGG TATTGGCCCGACGCAA <u>AT</u> GCCCGGGAGGC	5985
15	Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAT	GCCTCCCCGGGCATTGCGTCGCGGCCA <u>AT</u> ACCTCAACAGATCC ATCAGTGA <u>AA</u> TTGAT <u>AT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGGCGAGTTGA <u>ACT</u> CGTCA	5986
		CGGC <u>GGG</u> <u>A</u> ATCAATT	5987
		AATTGAT <u>AT</u> CCCGCCG	5988
		TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTACCGCA CCTACCTCGGCGGG <u>A</u> ATCAATT <u>C</u> ACTGATGGATCTGTTGAGG TATTGGCCCGACGCAA <u>AT</u> GCCCGGGAGGC	5989
		GCCTCCCCGGGCATTGCGTCGCGGCCA <u>AT</u> ACCTCAACAGATCC ATCAGTGA <u>AA</u> TTGAT <u>GT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGGCGAGTTGA <u>ACT</u> CGTCA	5990
20	Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAC	CGGC <u>GGG</u> <u>A</u> ATCAATT	5991
		AATTGAT <u>GT</u> CCCGCCG	5992
		CTTTCGGAGGAATTATGCTGATCTAATGAAGTCGCTGCCGTCA TTTGGGTGGTGG <u>A</u> <u>A</u> GGGACTCAGCTTCCCTCTCACAGCA CAAGGGCCACCCCTGCTGTTCTATTGGAGG	5993
		CCTCCAATAGGAACACAGCAGGGTGGCCCTTGCTTGAGAGG GAAAAGCTGAGTCCC <u>TT</u> ACCACCA <u>CC</u> AAAATGACGGCAGCGAC TTCATTAGGATCAGCATAATTCCCGAAAAG	5994
		TGGTGG <u>A</u> <u>A</u> GGGACTC	5995
25	Increased Starch ADPGPP <i>Zea mays</i> Thr96Lys ACC-AAA		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		GAGTCCCTTACCA	5996
5	Increased Starch ADPGPP <i>Zea mays</i> Pro124Leu CCC-CTC	CAAGCACAAGGGCCACCCCTGCTGTCCTATTGGAGGATGTACA GGCTTATTGATATCC T CATGAGCAACTGTTCAACAGTGGCATAAA CAAGATATTGTTATGACTCAGTCACTC	5997
		GAGTTGAAC TGAGTCATAACAAATATCTTGTTATGCCACTGTTGA AACAGTTGCTCATGAGGATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGTGGCCCTGTGCTT	5998
		TGATATCC T CATGAGCA	5999
		TGCTCATGAGGATATCA	6000
10	Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTCTTAACCGTCACATTCACTCGTAC CTATCTTGGTGGGA <u>A</u> ATCAACTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6001
		GCCTCCCCAGGCATTGTGTTGCAGCCAGCACCTAACAGATCCA TCAGTGAAGTTGATATTCCCACCAAGATAAGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAAC TGAGTC	6002
		TGGTGGGA <u>A</u> ATCAACT	6003
		AGTTGATATTCCCACCA	6004
15	Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTCTTAACCGTCACATTCACTCGTAC CTATCTTGGTGGGA <u>A</u> ACATCAACTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6005
		GCCTCCCCAGGCATTGTGTTGCAGCCAGCACCTAACAGATCCA TCAGTGAAGTTGATGTTCCCACCAAGATAAGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAAC TGAGTC	6006
		TGGTGGGA <u>A</u> ACATCAACT	6007
		AGTTGATGTTCCCACCA	6008
20	Increased Starch ADPGPP <i>Solanum tuberosum</i> Ala58Lys GCG-AAG	CTTGAGAGGCAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGG <u>A</u> AGGGAACTCGTCTTCCCCCTCACCAA ACGTCGTGCTAACGCTGCCGTTCCAATGGGAG	6009
		CTCCCATTGGAACGGCAGGCTTAGCACGACGTTGGTGGGGGG AAAAGACGAGTTCCC T CCCCCTCCTAGAATGATTGCTACTACTG TCCTTGATGCCCTCTTTGCCTCTCAAG	6010
		GAGGGGG <u>A</u> AGGGAACT	6011
		AGTTCCCTTCCCCCTC	6012
25	Increased Starch ADPGPP <i>Solanum tuberosum</i> Pro86Leu CCA-CTA	CCAAACGTCGTGCTAACGCTGCCGTTCCAATGGGAGGAGCATATA GGCTAATTGATGTACTAATGAGCAACTGTATTAACAGTGGCATAA CAAAGTATACTACATTCTCACTCAATTCAACTC	6013
		GAGTTGAATTGAGTGAGAATGTACTTTGTTGATGCCACTGTTAA TACAGTTGCTCATTAGTACATCAATTAGCCTATATGCTCCTCCAT TGGAACGGCAGGCTTAGCACGACGTTGG	6014

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAT	TGATGTACTAATGAGCA	6015
		TGCTCATTAGTACATCA	6016
		CTCAATTCAACTCAGCCTCACTTAACAGGCATATAAGCTCGTGCTTA CAACTTTGGCAATAATGTCACATTGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6017
		AATTCACCTGGTGTGAGTTGCTGCTAACAGACCTCGACATAGCCA CTCTCGAATGTGACATTATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGGCTGAGTTGAATTGAG	6018
		TGGCAATAATGTCACAT	6019
		ATGTGACATTATTGCCA	6020
	Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAC	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAAGCTCGTGCTTA CAACTTTGGCAATAACGTACATTGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6021
		AATTCACCTGGTGTGAGTTGCTGCTAACAGACCTCGACATAGCCA CTCTCGAATGTGACGTTATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGGCTGAGTTGAATTGAG	6022
		TGGCAATAACGTACAT	6023
		ATGTGACGTTATTGCCA	6024
		TATTTGAATCTCCAAAAGCTGACCCAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAAAGGGACTCGCCTTTCCCTTACTAGCA GGAGAGCTAACGCCAGCAGTGCCATTGGAGG	6025
10	Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAA	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGGCAGTCCCCTTACCAACCACCCAGCACAATTGCAGCCACA TTTTTGGGTCAAGCTTTGGAGATTCAAATA	6026
		TGGTGGTAAAGGGACTC	6027
		GAGTCCCCTTACCAACCA	6028
		TATTTGAATCTCCAAAAGCTGACCCAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAAACGGGACTCGCCTTTCCCTTACTAGCA GGAGAGCTAACGCCAGCAGTGCCATTGGAGG	6029
		CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGGCAGTCCCCTTACCAACCACCCAGCACAATTGCAGCCAC ATTTTTGGGTCAAGCTTTGGAGATTCAAATA	6030
15	Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAC	TGGTGGTAAACGGGACTC	6031
		GAGTCCCCTTACCAACCA	6032
		CTAGCAGGAGAGCTAACGCCAGCAGTGCCATTGGAGGGTGTAC	6033
		AGGCTGATTGATGTGCTATTGAGCAACTGCATCAACAGTGGCATT	
		AGAAAGATTTCAATTCTACCCAGTTCAATT	
20	Pro126Leu CCT-CTT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GAATTGAACTGGGTAAAGAATGAAAATCTTCTAATGCCACTGTTGA TGCAGTTGCTCAT <u>A</u> GCACATCAATCAGCCTGTAACACCCCTCAA TTGGCACTGCTGGCTTAGCTCTCGCTAG	6034
	TGATGTGCT <u>T</u> ATGAGCA	6035
	TGCTCAT <u>A</u> GCACATCA	6036
5 Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAT	CCCAGTTCAATT <u>C</u> GTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTGGAGATA <u>A</u> ATGTGAATTGGGGATGGCTTGTGGAGGTT	6037
	TTTGCTGCTACACAAACACCTGGAGAATC	
	GATTCTCCAGGTGTTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATT <u>C</u> AC <u>T</u> ATCTCCAAAATTATAGGTTCGAGCAAGAT	6038
	GACGATTAAGCGAAAACGAATTGAACTGGG	
	TGGAGATA <u>A</u> ATGTGAATT	6039
	AATT <u>C</u> AC <u>T</u> ATCTCCA	6040
10 Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAC	CCCAGTTCAATT <u>C</u> GTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTGGAGATA <u>A</u> CGTGAATTGGGGATGGCTTGTGGAGGTT	6041
	TTTGCTGCTACACAAACACCTGGAGAATC	
	GATTCTCCAGGTGTTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATT <u>C</u> AC <u>T</u> ATCTCCAAAATTATAGGTTCGAGCAAGAT	6042
	GACGATTAAGCGAAAACGAATTGAACTGGG	
	TGGAGATA <u>A</u> CGTGAATT	6043
	AATT <u>C</u> AC <u>T</u> ATCTCCA	6044

Table 21
Oligonucleotides to produce plants with waxy starch

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTCATAATGGCAACTGTGACTGCTTC TTCTAACTTGTGT <u>GAAGAAC</u> TTCACTTTCAACAATCATGGTGCTT CTTCATGCTCTGATGTCGCTCAGATTAC	6045
		GTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGA AAAGTGAAGTTCTT <u>CACACAAAG</u> TTAGAAGAAGCAGTCACAGTTGC CATTATGAACTACCCGTTACCTGGATT	6046
		CTTTGTGT <u>GAAGAAC</u> TT	6047
		AAGTTCTT <u>CACACAAAG</u>	6048
10	Waxy starch GBSS <i>Arabidopsis thaliana</i> Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTCATAATGGCAACTGTGACTGCTTCTT CTAACTTGTGT <u>CATGAAC</u> TTCACTTTCAACAATCATGGTGCTTCT TCATGCTCTGATGTCGCTCAGATTACCT	6049
		AGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTT GAAAAGTGAAGTT <u>CATGACACAAAG</u> TTAGAAGAAGCAGTCACAGTT GCCATTATGAACTACCCGTTACCTGGAT	6050
		TTGTGT <u>CATGAAC</u> TTCA	6051
		TGAAGTT <u>CATGACACAA</u>	6052
		TAAACGGGTAGTCATAATGGCAACTGTGACTGCTTCTTCAACTT TGTGT <u>CAAGAAC</u> TT <u>GACT</u> TTCAACAATCATGGTGCTTCTTCATGCT CTGATGTCGCTCAGATTACCTAAAAGG	6053
15	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	CCTTTAAGGTAAATCTGAGCGACATCAGAGCATGAAGAAGCACCAT GATTGTTGAAAGT <u>CAAGTT</u> TTGACACAAAGTTAGAAGAAGCAGT CACAGTTGCCATTATGAACTACCCGTTA	6054
		AAGAAC <u>TTGACT</u> TTCA	6055
		TGAAAAGT <u>CAAGTT</u> CTT	6056
		TGACTGCTTCTTCAACTTTGTGT <u>CAAGAAC</u> TTCACTTTCAACAAT CATGGTGCTTCTT <u>GATGCT</u> CTGATGTCGCTCAGATTACCTAAAAG GCCAATCCTTGACTCATTGTGGGTTAAG	6057
20	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser24Term TCA-TGA	CTTAACCCACAATGAGTCAAGGATTGGCCTTAAAGGTAA <u>CTGAG</u> CGACATCAGAGCAT <u>CAAGAAC</u> CCATGATTGTTGAAAAGTGAAGT TCTTGACACAAAGTTAGAAGAAGCAGTCA	6058
		TGCTTCTT <u>GATGCT</u> CTG	6059
		CAGAGCAT <u>CAAGAAC</u> CA	6060

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Arabidopsis thaliana</i> Cys25Term TGC-TGA	TGCTTCTTCAACTTGTGTCAAGAACCTCACTTTCAACAATCATG GTGCTTCTCATGATCTGATGTGTCGCTCAGATTACCTAAAAGGCCA ATCCTTGACTCATTGGGTTAAGGTCA	6061
		TGACCTTAACCCACAATGAGTCAGGATTGGCCTTTAAGGTAATC TGAGCGACATCAGATCATGAAGAAGCACCATTGATTGTTGAAAGTG AAGTTCTTGACACAAAGTTAGAAGAAGCA	6062
		TCTTCATGATCTGATGT	6063
		ACATCAGATCATGAAGA	6064
10	Waxy starch GBSS <i>Antirrhinum majus</i> Lys24Term AAA-TAA	GTAACAGCTTCACAGTGGTGTACATGTCCATGGTGGAGCAACG TCTTCACCGGATACTAAACAAACTTGGCCCAGGTTGGCCTCAGG AACCAGCAATTCACTACAATGGGTTGAGAT	6065
		ATCTCAACCCATTGTGAGTGAATTGCTGGTCCCTGAGGCCAACCT GGGCCAAGTTGTTAAAGTATCCGGTGAAGACGTTGCTCCACCAT GGACATGTGACACCAACTGTGAAGCTGTTAC	6066
		CGGATACTAAACAAAC	6067
		GTGGTTAAAGTATCCG	6068
15	Waxy starch GBSS <i>Antirrhinum majus</i> Leu27Term TTG-TAG	CACAGTTGGTGTACATGTCCATGGTGGAGCAACGTCTCACCGG ATACTAAAACAAACTAGGCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAAATGGGTTGAGATCAATAAACAT	6069
		ATGTTTATTGATCTAACCCATTGTGAGTGAATTGCTGGTCCCTGA GGCCAACCTGGGCTAGTTGTTTAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG	6070
		AACAAACTAGGCCAGG	6071
		CCTGGGCCAGTTGTT	6072
20	Waxy starch GBSS <i>Antirrhinum majus</i> Gln29Term CAG-TAG	TTGGTGTACATGTCCATGGTGGAGCAACGTCTCACCGGATACT AAAACAAACTGGCCTAGGTTGGCCTCAGGAACCAGCAATTCACT CACAAATGGGTTGAGATCAATAAACATGGTG	6073
		CAACCATGTTATTGATCTAACCCATTGTGAGTGAATTGCTGGTT CCTGAGGCCAACCTAGGCCAAGTTGTTAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA	6074
		ACTTGGCCAGTTGGC	6075
		GCCAACCTAGGCCAAGT	6076
25	Waxy starch GBSS <i>Antirrhinum majus</i> Gln35Term CAG-TAG	GGTGGAGCAACGTCTCACCGGATACTAAAACAAACTGGCCCAG GTTGGCCTCAGGAACCTAGCAATTCACTCACAAATGGGTTGAGATCAA TAAACATGGTTGATAAGCTTCAAATGAGGA	6077
		TCCTCATTGAAAGCTTATCAACCATGTTATTGATCTAACCCATTG TGAGTGAATTGCTAGTTCCCTGAGGCCAACCTGGCCAAGTTGTT TTAGTATCCGGTGAAGACGTTGCTCCACC	6078

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Antirrhinum majus</i> Gln36Term CAA-TAA	TCAGGAAC <u>T</u> AGCAATT	6079
		GAATTG <u>C</u> TAGTTCCCTGA	6080
		GGAGCAACGTCTCACCGGATACTAAAACAAACTTGGCCCAGGTT GGCCTCAGGAACC <u>A</u> ATTCACTCACAAATGGGTTGAGATCAATAA ACATGGTTGATAAGCTCAAATGAGGAACA	6081
		TGTTCC <u>T</u> CATTGAAGCTTATCAACC <u>A</u> TGTTATTGATCTCAACCCA TTGTGAGTGAATT <u>A</u> CTGGTTCTGAGGCCAAC <u>C</u> TTGGGCCAAGTTT	6082
		GTTTAGTATCCGGTGAAGACGTTGCTCC GGAACC <u>A</u> GTAA <u>T</u> CACT	6083
		AGTGAATT <u>A</u> CTGGTTCC	6084
	Waxy starch GBSS <i>Ipomoea batatas</i> Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTGTTCATGTCTGTG GGGGTGCC <u>A</u> CTTCT <u>T</u> GAGAATCAAAGTGGGTTGGGTC <u>A</u> TTAG CCCTGAGGAGCCAAG <u>C</u> GTGACTCACAATG	6085
		CATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATTGACCCACC CCACTTTGATT <u>CTC</u> <u>A</u> AGAAGTGGCACCCCCACAGACATGAGAAA CAAAGTGTGAGGCAGTTATAGTCGCCATCAC	6086
		CCACTTCT <u>T</u> GAGAATCA	6087
		TGATTCT <u>C</u> <u>A</u> AGAAGTGG	6088
		ATGGCGACTATAACTGCCTCACACTTGTTCATGTCTGTGGGG GTGCCACTTCTGG <u>A</u> ATCAAAGTGGGTTGGGTC <u>A</u> TTAGCC TGAGGAGCCAAG <u>C</u> GTGACTCACAATGGGT	6089
10	Waxy starch GBSS <i>Ipomoea batatas</i> Glu21Term GAA-TAA	ACCCATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATTGACCC ACCCCCACTTTGATT <u>ATCC</u> CAGAAGTGGCACCCCCACAGACATGAG AAACAAAGTGTGAGGCAGTTATAGTCGCCAT	6090
		CTTCTGG <u>A</u> ATCAAA	6091
		TTTGATT <u>ATCC</u> CAGAAG	6092
		CGACTATAACTGCCTCACACTTGTTCATGTCTGTGGGGTGC CACTTCTGG <u>A</u> ATGAAAGTGGGTTGGGTC <u>A</u> TTAGCC <u>C</u> TGAG GAGCCAAG <u>C</u> GTGACTCACAATGGGTTGAG	6093
		CTCAACCCATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATTGA CCCAACCCCCACTTT <u>C</u> ATTCTCCAGAAGTGGCACCCCCACAGACA TGAGAAACAAAGTGTGAGGCAGTTATAGTCG	6094
15	Waxy starch GBSS <i>Ipomoea batatas</i> Ser22Term TCA-TGA	TGG <u>G</u> AGAAT <u>G</u> AAAGTGG	6095
		CCACTTT <u>C</u> ATTCTCCA	6096

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Ipomoea batatas</i> Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTGTTCATGTCGTGGGGTGCCA CTTCTGGAGAACAT <u>A</u> AGTGGGGTGGTCAATTAGCCCTGAGGA GCCAAGCTGTGACTCACAATGGGTGAGAC	6097
		GTCTCAACCCATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATT GACCCAACCCCAC <u>T</u> ATGATTCTCCAGAAGTGGCACCCCCACAGA CATGAGAAACAAAGTGTGAGGCAGTTAGT	6098
		GAGAACAT <u>A</u> AGTGGGG	6099
		CCCCACTT <u>A</u> TGATTCTC	6100
		CCTCACACTTGTTCATGTCGTGGGGTGCCACTTCTGGAGA ATCAAAAGTGGGT <u>A</u> GGTCATTAGCCCTGAGGAGCCAAGCTGT GACTCACAATGGGTGAGACCTGTGAACAA	6101
10	Waxy starch GBSS <i>Ipomoea batatas</i> Leu26Term TTG-TAG	TTGTTCACAGGTCTCAACCCATTGTGAGTCACAGCTGGCTCCTCA GGGCTAATTGACC <u>T</u> ACCCCAC <u>T</u> TTGATTCTCCAGAAGTGGCAC CCCCACAGACATGAGAAACAAAGTGTGAGG	6102
		AGTGGGGT <u>A</u> GGGTCAAT	6103
		ATTGACC <u>C</u> CTACCCACT	6104
		CATCGCGATTGGCTCCTACTGCTCTCACAGAACGGAAC GGTGACGGGTCT <u>A</u> GGTGGTGTGAGAACAGCGCGTGCCTCAATT CCAGGGAAAGAACAGAACGCCAACGTGAATTCA	6105
		TGAATTCACTTGGCTCTGTTCCCTGGGAATTGAAGCAGCG CTTCTCGACACC <u>C</u> TAAGACCCCGTCACCGTTGCCATTCTGTGA GAGAGCAGTAAGGAGAACATGCCGATG	6106
15	Waxy starch GBSS <i>Astragalus membranaeus</i> Tyr8Term TAT-TAG	GGGTCT <u>T</u> AGGTGGTGTC	6107
		GACACCAC <u>C</u> TAAGACCC	6108
		ATTGTTGCTCCTACTGCTCTCACAGAACGGTGACGG GGTCTTATGTGGT <u>T</u> AGAGAACAGCGCGTGCCTCAATTCCAGGGAA GAACAGAACCCAAAGTGAATTCACCTCAGAA	6109
		TTCTGAGGTGAATTCACTTGGCTCTGTTCCCTGGGAATTGA AGCACCGCGCTCT <u>C</u> TACACCACATAAGACCCCGTCACCGTTGCCA TTCTGTGAGAGAGCAGTAAGGAGAACAAAT	6110
		TGTGGTGT <u>A</u> AGAGAACGCG	6111
20	Waxy starch GBSS <i>Astragalus membranaeus</i> Ser11Term TCG-TAG	CGCTTCT <u>C</u> TACACCACAA	6112

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Astragalus membranaeus</i> Arg12Term AGA-TGA	TGTTGCTCCTTACTGCTCTCACAGAACGGTGACGGGG TCTTATGTGGTGT <u>CGTGAAGCGCGT</u> GCTCAATTCCCAGGGAAAGA ACAGAACGCCAAAGTGAATT <u>CACCTCAGAAGA</u>	6113
		TCTTCTGAGGTGAATT <u>ACTTGGCTTCTGTTCCCTGGGAATT</u> GAAGCACGCGCTTC <u>ACGACACCACATAA</u> GACCCCCGTACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA	6114
		TGGTGT <u>CGTGAAGCGCG</u>	6115
		CGCGCTTC <u>ACGACACCA</u>	6116
10	Waxy starch GBSS <i>Astragalus membranaeus</i> Cys15Term TGC-TGA	ACTGCTCTCACAGAACGGCAACGGTGACGGGGCTTATGTGGT GTCGAGAACGCG <u>GATTCAATTCCCAGGGAAAGAACAGAACCAA</u> AGTGAATT <u>CACCTCAGAAGATAATCTCA</u> AT	6117
		ATTGAGATT <u>TATCTTGAGGTGAATT</u> ACTTGGCTTCTGTTCTC CCTGGGAATT <u>GAATCACGCGCTTCTCGACACCACATAA</u> GACCCCCG TCACCGTTGCCATT <u>CTGTGAGAGAGCAGT</u>	6118
		AGCGCGT <u>GATTCAATT</u> C	6119
		GAATT <u>GAATCACGCGCT</u>	6120
		CACAGAACGGCAACGGTGACGGGGCTTATGTGGT <u>CGAGAACG</u> GCGT <u>GCTCAATTCC</u> TAGGGAAAGAACAGAACGCCAAAGTGAATT <u>CA</u> CCTCAGAAC <u>ATAATCTCAATAGCCAAGCAT</u>	6121
15	Waxy starch GBSS <i>Astragalus membranaeus</i> Gln19Term CAG-TAG	ATGCTTG <u>GCTATTGAGATT</u> TCTTGAGGTGAATT <u>ACTTGGCT</u> TCTGTT <u>CTCCCTAGGAATT</u> GAAGCACGCGCTTCTCGACACCACAT AAGACCCCCGT <u>ACCGTTGCCATTCTGTG</u>	6122
		TCAATT <u>CCTAGGGAAAGA</u>	6123
		TCTTCC <u>CTAGGAATTGA</u>	6124
		TGTA <u>GCTTAGACCACACATCACATGGC</u> AAGCATCACAG <u>CTTGACACCAC</u> TTGT <u>CAAGAACCTTCA</u> CTAGACACC <u>AAATCAACCTTGT</u> CACAGAT	6125
20	Waxy starch GBSS <i>Solanum tuberosum</i> Ser7Term TCA-TGA	ATCTGT <u>GACAAGGTTGATTGGTGT</u> CTAGTGAAG <u>TTGGCTTCTG</u> ACACAA <u>AGGGTGTCAAGCTGTGATGCTGCCATGTGATGTG</u> TCTACAAA <u>AGGGGAATCTACCAAGCTACA</u> CACAG <u>CTTGACACCACT</u>	6126
		AGTGGTGT <u>CAAGCTGT</u>	6127
		AGTGGTGT <u>CAAGCTGT</u>	6128
		TCCCC <u>TTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC</u> ACACCA <u>CTTGTGTGAAGAACCCAAACTTCA</u> CT <u>ACTAGACACCAAA</u> AT <u>CA</u> ACCTTG <u>TCACAGATAGGACTCAGGAACCA</u>	6129
25	Waxy starch GBSS <i>Solanum tuberosum</i> Ser12Term TCA-TGA	TGGTT <u>CCCTGAGTCCTATCTGTGACAAGGTTGATTGGTGT</u> TAGT <u>G</u> AAGTT <u>GGCTTCTCACACAAAGTGGTGTGAAGCTGTGATGCTTGC</u> CATGT <u>GATGTGGT</u> CTACAAA <u>AGGGGA</u>	6130

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5		CTTTGTGT <u>G</u> AAGAACCC	6131
		GGCTTCTT <u>C</u> ACACAAAG	6132
	Waxy starch GBSS <i>Solanum tuberosum</i> Arg13Term AGA-TGA	CCCTTTTGAGACCACACATCACATGGCAAGCATCACAGCTTCAC ACCACTTTGTGT <u>C</u> ATGAAGCCAAACTCAGTACAGACACCAAATCAAC CTTGTACAGATAGGACTCAGGAACCATA	6133
		TATGGTTCTGAGTCCTATCTGTGACAAGGTTGATTGGTGTCTAG TGAAGTTGGCTT <u>C</u> ATGACACAAAGTGGTGTGAAGCTGTGATGCTT GCCATGTGATGTGGTCTACAAAAAGGG	6134
		TTGTGT <u>C</u> ATGAAGCCAA	6135
		TTGGCTT <u>C</u> ATGACACAA	6136
		TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACT TTGTGT <u>C</u> AAAGCTAAACTTCACTAGACACCAAATCAACCTTGTCA ACAGATAGGACTCAGGAACCATACTCTGA	6137
	<i>Solanum tuberosum</i> Gln15Term CAA-TAA	TCAGAGTATGGTTCTGAGTCCTATCTGTGACAAGGTTGATTGGT GTCTAGTGAAGTT <u>A</u> GCTTCTTGACACAAAGTGGTGTGAAGCTGTG ATGCTGCCATGTGATGTGGTCTACAA	6138
		CAAGAAG <u>C</u> TAAACTCA	6139
		TGAAGTT <u>A</u> GCTTCTTG	6140
		CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTGTGT AAGAAGCCAAACT <u>T</u> GACTAGACACCAAATCAACCTTGTACAGATA GGA <u>T</u> CTCAGGAACCATACTCTGA <u>T</u> CTCACAA	6141
10	Waxy starch GBSS <i>Solanum tuberosum</i> Ser17Term TCA-TGA	TTGTGAGTCAGAGTATGGTTCTGAGTCCTATCTGTGACAAGGTTG ATTGGTGTCTAGT <u>C</u> AAAGTTGGCTTCTTGACACAAAGTGGTGTGA AGCTGTGATGCTGCCATGTGATGTGG	6142
		CCAAACT <u>T</u> GACTAGACA	6143
		TGTCTAGT <u>C</u> AAAGTTGG	6144
		GT <u>C</u> GATCACTCTCTCACCGCCGAAACAGATTGACACAAAAA TGGCAACATAACGT <u>G</u> ATCTCAATGCCGACGAGAACCGCGTGCT TCAATTACCAAGGAAGATCAGCAGAGTCTA	6145
		TAGACTCTGCTGATCTCTGGTAATT <u>G</u> AAGCACGCCGGTCTCGT CGGCATTGAAGAT <u>C</u> ACGTTATTGGCCATTGGTGTCAAATCT GTTTGGCGGTGAGAGAGAGTGTGAC	6146
15	Waxy starch GBSS <i>Pisum sativum</i> Gly6Term GGA-TGA	CAATAACGT <u>G</u> ATCTCA	6147
		TGAAGAT <u>C</u> ACGTTATTG	6148

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Pisum sativum</i> Ser8Term TCA-TGA	ACTCTTCTCTCACCGCCGAAACAGATTTGACACAAAAATGGCAAC ATAACGGGATCTT <u>G</u> AATGCCGACGAGAACCGCGTGCTCAATT CCAAGGAAGATCAGCAGAGTCTAAACTGAA	6149
		TTCAGTTAGACTCTGCTGATCTCCTTGGTAATTGAAGCACGCGG TTCTCGTGGCATT <u>C</u> AAGATCCCCTATTGTGCCATTGGTGC AAAATCTGTTCGGCGGTGAGAGAAGAGT	6150
		GGGATCTT <u>G</u> AATGCCGA	6151
		TCGGCATT <u>C</u> AAGATCCC	6152
10	Waxy starch GBSS <i>Pisum sativum</i> Arg12Term AGA-TGA	ACCGCCGAAACAGATTTGACACAAAAATGGCAACAATAACGGGAT CTTCAATGCCGACGT <u>G</u> AACCGCGTGCTCAATTACCAAGGAAGAT CAGCAGAGTCTAAACTGAATT <u>G</u> CCTCAGA	6153
		TCTGAGGCAAATT <u>C</u> AGTTAGACTCTGCTGATCTCCTTGGTAATT GAAGCACCGCGGTT <u>C</u> ACGTGGCATTGAAGATCCCCTATTGTGC CATTTTGTCAAAATCTGTTGGCGGT	6154
		TGCCGACGT <u>G</u> AACCGCG	6155
		CGCGGTT <u>C</u> ACGTGGCA	6156
		AGATTTGACACAAAAATGGCAACAATAACGGGATCTCAATGCCG ACGAGAACCGCGTG <u>A</u> TTCAATTACCAAGGAAGATCAGCAGAGTCT AAACTGAATT <u>G</u> CCTCAGATACTTCAT	6157
15	Waxy starch GBSS <i>Pisum sativum</i> Cys15Term TGC-TGA	ATTGAAGTGTATCTGAGGCAAATT <u>C</u> AGTTAGACTCTGCTGATCTT CCTGGTAATT <u>G</u> AAT <u>C</u> ACCGCGGTT <u>T</u> CGTGGCATTGAAGATCCC GTTATTGTGCCATTGGTGTCAAATCT	6158
		ACCGCGTG <u>A</u> TTCAATT	6159
		TAATT <u>G</u> AAT <u>C</u> ACCGCGGT	6160
		CACAAAAATGGCAACAATAACGGGATCTCAATGCCGACGAGAAC CGCGTGCTCAATT <u>A</u> GGCAAGGAAGATCAGCAGAGTCTAAACTGAAT TTGCCCTCAGATACTTCATAACAACCAA	6161
20	Waxy starch GBSS <i>Pisum sativum</i> Tyr18Term TAC-TAG	TTGGTTGTTATTGAAGTGTATCTGAGGCAAATT <u>C</u> AGTTAGACTCTG CTGATCTCCTTG <u>C</u> TAATTGAAGCACCGCGGTT <u>T</u> CGTGGCATTGA AGATCCCCTATTGTGCCATTGGTGC	6162
		TTCAATT <u>A</u> GGGAAG	6163
		CTTCCTTG <u>C</u> TAATTGAA	6164
		TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATT TCGTTCCAGGAGCT <u>G</u> ACACTGAGCATCCATGCATTAGAGACTAA GGCTAATAATTGTCTCACACTGGACCCCTG	6165
25	Waxy starch GBSS <i>Manihot esculenta</i> Ser14Term TCA-TGA	CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTAATGCAT GGATGCTCAAGTGT <u>C</u> AGCTCCTGGAAACGAAATGTGCAGCTATT CAGTTGCCATGGTGTCTCTCCGGTGTAGA	6166

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ / ID NO.
5		CAGGAGCT <u>GACACTTGA</u>	6167
		TCAAGTGT <u>CAGCTCCTG</u>	6168
	Waxy starch GBSS <i>Manihot esculenta</i> Leu16Term TTG-TAG	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCGTT CCAGGAGCTCACACT <u>AGAGCATCCATGCATTAGAGACTAAGGCTA</u> ATAATTGTCACACTGGACCCTGGACCCA	6169
		TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTAGTCTCTA ATGCATGGATGCT <u>CTAGTGTGAGCTCTGGAAACGAAATGTGCAG</u> CTATTACAGTGCATGGTGCTCTCCGG	6170
		CTCACACT <u>AGAGCATCC</u>	6171
		GGATGCT <u>CTAGTGTGAG</u>	6172
		TGGCAACTGTAATAGCTGCACATTTCGTTCCAGGAGCTCACACTT GAGCATCCATGCAT <u>GAGAGACTAAGGCTAATAATTGTCACACT</u> GGACCCCTGGACCCAAACTATCACTCCCAA	6173
	<i>Manihot esculenta</i> Leu21Term TTA-TGA	TTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAGACAAATTAA TTAGCCTTAGTCT <u>CTCATGCATGGATGCTCAAGTGTGAGCTCCTGG</u> AAACGAAATGTGCAGCTATTACAGTTGCCA	6174
		CCATGCAT <u>GAGAGACTA</u>	6175
		TAGTCT <u>CTCATGCATGG</u>	6176
		GCAACTGTAATAGCTGCACATTTCGTTCCAGGAGCTCACACTTGA GCATCCATGCATT <u>ATAGACTAAGGCTAATAATTGTCACACTGG</u> ACCCCTGGACCCAAACTATCACTCCCAATG	6177
15	Waxy starch GBSS <i>Manihot esculenta</i> Glu22Term GAG-TAG	CATTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAGACAAAT TATTAGCCTTAGT <u>CTATAATGCATGGATGCTCAAGTGTGAGCTCCT</u> GGAAACGAAATGTGCAGCTATTACAGTTGC	6178
		ATGCATT <u>ATAGACTAAG</u>	6179
		CTTAGT <u>CTATAATGCAT</u>	6180
		GTAATAGCTGCACATTTCGTTCCAGGAGCTCACACTTGAGCATCC ATGCATTAGAGACT <u>TAAGGCTAATAATTGTCACACTGGACCCTG</u> GACCCAAACTATCACTCCCAATGGTTAA	6181
		TTAACCAATTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAG ACAAATTATTAGCCT <u>TAAGTCTCTAATGCATGGATGCTCAAGTGTGA</u> GCTCCTGGAAACGAAATGTGCAGCTATTAC	6182
20	Waxy starch GBSS <i>Manihot esculenta</i> Lys24Term AAG-TAG	TAGAGACT <u>TAAGGCTAAT</u>	6183
		ATTAGCCT <u>TAAGTCTCTA</u>	6184

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Phaseolus vulgaris</i> Ser12Term TCA-TGA	ACAACTCCTCCGTACCGGTATAAGCATGGCAACGGTATCGATGG CATCGTGGTGGCGTGAAAAGGCCGTGGAGTACAGAGACAAAAA GTGAAATCTCGGGTCAGATGAGCCTGAACCG	6185
		CGGTTCAAGGCTCATCTGACCCGAAGATTCACTTTGTCTGTAC TCCACGCCCTTTCACGCCACGCACGATGCCATCGATACCGTTG CCATGCTTATACCGGTGACGGAGGAGTTG	6186
		CGTGGCGTGAAAAGGCG	6187
		CGCCTTTCACGCCACG	6188
10	Waxy starch GBSS <i>Phaseolus vulgaris</i> Trp16Term TGG-TGA	CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCCTGGC GTCAAAAGGCGCGTGAAAGTACAGAGACAAAAGTGAATCTCGGG TCAGATGAGCCTGAACCGTCATGAATTGAAA	6189
		TTCAATTATGACGGTTCAAGGCTCATCTGACCCGAAGATTCACT TTTGTCTCTGTACTCACGCCCTTTGACGCCACGCACGATGCC ATCGATACCGTTGCCATGCTTACCGGTG	6190
		GGCGCGTGAAAGTACAGA	6191
		TCTGTACTCACGCC	6192
		ATAAGCATGGCAACGGTATCGATGGCATCGTGCCTGGCGTCAAA GGCGCGTGGAGTACATAGACAAAAGTGAATCTCGGGTCAGATG AGCCTGAACCGTCATGAATTGAAATACGATG	6193
15	Waxy starch GBSS <i>Phaseolus vulgaris</i> Glu19Term GAG-TAG	CATCGTATTCAATTATGACGGTTCAAGGCTCATCTGACCCGAAGA TTTCACTTTGTCTATGTACTCACGCCCTTTGACGCCACGCAC GATGCCATCGATACCGTTGCCATGCTTAT	6194
		GGAGTACATAGACAAAA	6195
		TTTGTCTATGTACTCC	6196
		ATGGCAACGGTATCGATGGCATCGTGCCTGGCGTCAAAAGGCC GTGGAGTACAGAGACATAAGTGAATCTCGGGTCAGATGAGCCT GAACCGTCATGAATTGAAATACGATGGGTGA	6197
		TCAACCCATCGTATTCAATTATGACGGTTCAAGGCTCATCTGACC CGAAGATTCACTTATGTCTCTGTACTCACGCCCTTTGACGCC ACGCACGATGCCATCGATACCGTTGCCAT	6198
20	Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys21Term AAA-TAA	CAGAGACATAAGTGA TTTCACTTATGTCTCTG	6199 6200
		ACGGTATCGATGGCATCGTGCCTGGCGTCAAAAGGCCGTGGAG TACAGAGACAAAAGTGTAAATCTCGGGTCAGATGAGCCTGAACCG TCATGAATTGAAATACGATGGGTGAGATCTC	6201
		GAGATCTCAACCCATCGTATTCAATTATGACGGTTCAAGGCTCAT CTGACCCGAAGATTACACTTTGTCTCTGTACTCACGCCCTTT GACGCCACGCACGATGCCATCGATACCGT	6202

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5		CAAAAGTGTAAATCTTCG	6203
		CGAAGATT <u>A</u> ACTTTTG	6204
	Waxy starch GBSS <i>Triticum aestivum</i> Tyr7Term TAT-TAG	GCGCCTAGCTCGAAAAGGTCGTCAATTGAGAGGGCTGCACCAATGG GTTCCATTCTTAATT <u>A</u> GTGTTCTTATCAAACAAACAGTGTGGTTCA CTGAAACTGTGCGCCTCACATCCAATTCCAG	6205
		CTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTTT GTTTGATAAGAAC <u>A</u> CTAATTAGGAATGGAACCCATTGGTGCAGCCT CTCAATGACGACCTTTGAGCTAGGCCG	6206
		CCTAATT <u>A</u> GTGTTCTTA	6207
		TAAGAAC <u>A</u> CTAATTAGG	6208
		CCTAGCTCGAAAAGGTCGTCAATTGAGAGGGCTGCACCAATGGGTT CATTCTTAATTATT <u>G</u> ATCTTATCAAACAAACAGTGTGGTTCACTGA AACTGTGCGCCTCACATCCAATTCCAGCAA	6209
	<i>Triticum aestivum</i> Cys8Term TGT-TGA	TTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACT GTTTGTTGATAAG <u>A</u> CTAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTGAGCTAGG	6210
		AATTATT <u>G</u> ATCTTATCA	6211
		TGATAAG <u>A</u> CTAATAATT	6212
		TCGAAAAGGTCGTCAATTGAGAGGGCTGCACCAATGGGTTCCATTCC TAATTATTGTTCTTA <u>G</u> CAAACAAACAGTGTGGTTCACTGAAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT	6213
15	Waxy starch GBSS <i>Triticum aestivum</i> Tyr10Term TAT-TAG	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACC AACACTGTTGTT <u>G</u> TAAGAACAAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTGCA	6214
		TGTTCTTA <u>G</u> CAAACAAA	6215
		TTTGTT <u>G</u> TAAGAACAA	6216
		CGAAAAGGTCGTCAATTGAGAGGGCTGCACCAATGGGTTCCATTCT AATTATTGTTCTTAT <u>A</u> AAACAAACAGTGTGGTTCACTGAAACTGTC GCCTCACATCCAATTCCAGCAATCTTGT	6217
		TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAAC CAACACTGTTGTT <u>A</u> AAAGAACAAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTGCA	6218
20	Waxy starch GBSS <i>Triticum aestivum</i> Gln11Term CAA-TAA	GTTCTTAT <u>A</u> AAACAAAC	6219
		TTTGTT <u>A</u> AAAGAAC	6220

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Triticum aestivum</i> Ser17Term TCA-TGA	AGGCTGCACCAATGGGTTCCATTCTAATTATTGTTCTTATCAAACA AACAGTGTGGTT <u>GACTGAAACTGTCGCTCACATCCAATTCCAGC</u> AATCTTGTAAACAATGAAGTTATGTTCT	6221
		AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAG GCGACAGTTTCAGT <u>CAACCAACACTGTTGTTGATAAGAACATA</u> ATTAGGAATGGAACCCATTGGTGCAGCCT	6222
		TGTTGGTT <u>GACTGAAAC</u>	6223
		GTTCAGT <u>CAACCAACA</u>	6224
10	Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	CAGCTGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTT <u>TAGGGCGTGAGGCCCGGAGGCCCGGCG</u> GATGCCGCTCTGGCATGAGGACCGTCGGAGCTA	6225
		TAGCTCCGACGGTCTCATGCCGAGAGCCGCATCCGCCGGGCTC CGGGGCCTCACGCCCT <u>A</u> GAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6226
		CAGGTT <u>TAGGGCGTG</u>	6227
		CACGCCCT <u>A</u> GAAACCTG	6228
		GGTTCCAGGGCGTGAGGCCCGGAGGCCGGGATGCGGCTC TCGGCATGAGGACCGT <u>C</u> TGAGCTAGCGCCGCCAACGCAAAGC CGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	6229
15	Waxy starch GBSS <i>Triticum aestivum</i> Gly46Term GGA-TGA	AGAGGCACCGCCGGGTCCC CGGGTGC GCGCTTCCGGCTTGC GTT GGGGCGGGC TAGCT <u>C</u> AGACGGTCTCATGCCGAGAGCCGCATC CGCCGGGCTCCGGG CTCACGCCCTGGAAACC	6230
		GGACCGT <u>C</u> TGAGCTAGC	6231
		GCTAGCT <u>C</u> AGACGGTCC	6232
		CGGAGCCCGCGGATGCGGCTCTGGCATGAGGACCGTCGGAG CTAGCGCCGCCCAACG <u>TAAAGCCGAAAGCGCACC CGCGGACC</u>	6233
		CGGC GG TGCC TCTCC ATGGTGGTGC GCG CC ACCG CGGTGGCGCGACCACCATGGAGAGGCACCGCCGGGCTCCCG GTGCGCTTCCGGCTT <u>A</u> CGTTGGGCGCGCTAGCTCCGACGG TCCTCATGCCGAGAGCCGCATCCGCCGGCTCCG	6234
20	Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CCCCAACG <u>TAAAGCCG</u>	6235
		CCGGCTT <u>A</u> CGTTGGGG	6236
		GC GG ATGCGGCTCTGGCATGAGGACCGTCGGAGCTAGCGCCG CCCCAACGCAAAAGCCGG <u>T</u> AAGCGCACC CGCGGACC CGCGG CCTCTCCATGGTGGTGC GCG CC ACCGG CAGCGCG	6237
		CGCCGCTGCCGGTGGCGCGACCACCATGGAGAGGCACCGCCG GGTCCC CGGGTGC GCG CT <u>T</u> ACCGGCTTGC GTTGGGCGGCG CTCCGACGGTCTCATGCCGAGAGCCGCATCCGC	6238
25			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Triticum aestivum</i> Glu85Term GAG-TAG	AAAGCCGGTAAGCGCAC	6239
		GTGCGCTTACCGGCTT	6240
		CTCTCCATGGTGGTGCACGCCACCGCAGCGGGCATGAACCT CGTGTTCGTCGGCGCCTAGATGGCGCCCTGGAGCAAGACCAGCG GCCTCGGCACGTCTCGGGGCTCCCCCAG	6241
		CTGGGGGGAGGCCCCCGAGGACGTGCGAGGCGCCGGTCTT GCTCCAGGGCGCCATCTAGGCGCCGACGAACACGAGGTTATGC CGCCGCTGCCGGTGGCGCGACCCATGGAGAG	6242
		TCGGCGCCTAGATGGCG	6243
		CGCCATCTAGGCGCCGA	6244
	Waxy starch GBSS <i>Triticum aestivum</i> Gln8Term CAG-TAG	GTCGTCTCTCGCTGCAGGTAGCCACACCCCTGCACGCGATGGC GGCTCTGGTCACGTCGTAGCTGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGCAGGTTTC	6245
		GAAAACCTGCACGCCCGAACCTGTCGGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCTACGACGTGACCAAGAGCCGCCATCGCGC GCGCAGGGTGTGGTACCTGCAGCGAGAGACGAC	6246
		TCACGTCGTAGCTGCC	6247
		GGCGAGCTACGACGTGA	6248
		CAGCTGCCACCTCCGGCACCGCTCTGGCATACCGACAGGTT CCGGCGTCAGGTTTAGGGTGTGAGGCCCGGAGCCCGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6249
10	Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	TCGCTCCGGTAGTCCTCATGCCGAGCGGCATCTGCCGGGCTC CGGGGCCTCACACCCATAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6250
		CAGGTTTTAGGGTGTG	6251
		CACACCCATAAAACCTG	6252
	Waxy starch GBSS <i>Triticum aestivum</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGAGATGCCGCTCGGCATGAGGACTACCG GAGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGCAGC	6253
		CGCGCACCAACATGGAGAGGGACCGGCCGGTCCCGCGGTGC TTCCCGGCTTGTGCTACGGGGCGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGCGCATCTGCCGGCTCCGGGG	6254
		CCGCCCCGTAGCAACAA	6255
		TTGTTGCTACGGGGCGG	6256

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGAAGTAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCATGGTGGTGCACCGCCA	6257
		TGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCGGTG CGCTTCCGGCTTTGTTACTTCGGGCGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGCGCATCTGCCGGCTCCG	6258
		CCCCGAAGTAACAAAGC	6259
		GCTTGTTACTTCGGGG	6260
10	Waxy starch GBSS <i>Triticum aestivum</i> Gln54Term CAA-TAA	AGCCCAGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGAAGCAATAAAAGCCGAAAGCGCACCGCGGAC CCGGCGGTGCCTCTCATGGTGGTGCACCGCCA	6261
		CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTTTATTGCTCGGGCGCGCTCGCTCCGG TAGTCCTCATGCCGAGCGCGCATCTGCCGGCT	6262
		CGAAGCAATAAAAGCCGG	6263
		CCGGCTTATTGCTTCG	6264
		CAGCTGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTCTAGGGCGTGAGGCCCGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	6265
15	Waxy starch GBSS <i>Triticum durum</i> Gln28Term CAG-TAG	TCGCTCCGATAGTCCTCATGACGAGGGCGCATCCGCCGGTTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCAGGAGGTGGCGAGCTG	6266
		CAGGTTCTAGGGCGTG	6267
		CACGCCCTAGAAACCTG	6268
		CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCGTAGCAAAGCCGAAAGCGCACCGCGG AGCCGGCGGTGCCTCTCATGGTGGTGCACCGCCA	6269
		TGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCGGTG CGCTTCCGGCTTGCTACGGGGCGCGCTCGCTCCGATAGTCC TCATGACGAGGGCCGATCCGCCGGTCCGGGG	6270
20	Waxy starch GBSS <i>Triticum durum</i> Lys52Term AAG-TAG	CCGCCCCGTAGCAAAGC	6271
		GCTTGCTACGGGGCGG	6272
		CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCGAAGTAAAGCCGAAAGCGCACCGCGGGAGC CGGCGGTGCCTCTCATGGTGGTGCACCGCCA	6273
		CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTTACTTCGGGCGCGCTCGCTCCGATAG TCCTCATGACGAGGGCCGATCCGCCGGTCCG	6274

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5		CCCCGAAG <u>TAAAGCCGG</u>	6275
		CCGGCTT <u>ACTTCGGGG</u>	6276
	Waxy starch GBSS <i>Triticum durum</i> Lys56Term AAA-TAA	GCGGATGCCGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC CCCAGCAAAGCCGG <u>TAAAGCGCACCGCGGGAGCCGGCGGTGC</u> CTCTCCATGGTGGTGC <u>CGCCACGGCAGCGGCG</u>	6277
		CGCCGCTGCCGTGGCGCGCACCA <u>CTGGAGAGGGACC</u> GGCG GCTCCCGCGGTGC <u>CTTACCGGCTTGCTCGGGCGGC</u> CTCG CTCCGATA <u>GT</u> CCTCATGACGAGGGCCGATCCGC	6278
		AAAGCCGG <u>TAAAGCGCAC</u>	6279
		GTGCGCT <u>ACCGGCTT</u>	6280
		TATCGGAGCGAGCGCCGCCCGAAGCAAAGCCGGAAAGCGCAC GCGGGAGCCGGCGGT <u>GACT</u> CTCCATGGTGGTGC <u>CGCCAC</u> GG CAGCGGCGGCATGAAC <u>CTCGT</u> TT <u>CGTCGGCG</u>	6281
	Waxy starch GBSS <i>Triticum durum</i> Cys64Term TGC-TGA	GGCGCCGAC <u>ACACGAGGTT</u> CATGCCGCC <u>GTGCCCGTGGCG</u> CGCACCA <u>CCATGGAGAGT</u> CACCGCCGG <u>CTCCCGGGTGC</u> GCTT CCGGCTT <u>GCTTCGGGCGGC</u> CTCG <u>CTCCGATA</u>	6282
		CGGCGGT <u>GACT</u> CTCCAT	6283
		ATGGAGAG <u>TACCGCCG</u>	6284
		CAGCTGCCAC <u>CTCCGGCACCGT</u> CC <u>GGCATCACCGACAGGTT</u> CCGGCGTGC <u>AGGTTT</u> <u>TAGGGTGTGAGGCCCCGGAGCCGGCAG</u> AT <u>GC</u> CGCC <u>GT</u> CG <u>GCATGAGGACTACCGGAGCGA</u>	6285
		TCGCTCCGGTAG <u>TCTCATGCCGAGCGGGC</u> AT <u>CTGCCGGG</u> CTC CGGGGC <u>CTCACACCT</u> <u>AAAAACCTG</u> CACGCCGG <u>ACCTGTC</u> GGT GATGCCGAGGACGGTGC <u>CCGGAGGTGGCGAGCTG</u>	6286
15	Waxy starch GBSS <i>Triticum turgidum</i> Gln28Term CAG-TAG	CAGG <u>TTT</u> <u>TAGGGTGTG</u>	6287
		CACAC <u>CCCT</u> <u>AAAAACCTG</u>	6288
		CCCCGGAGCCGGCAGAT <u>GC</u> GCC <u>GT</u> CG <u>GCATGAGGACTACCG</u> GAGCGAGCGCCGCC <u>CGTAGCAACAAAGCCGGAAAGCGCACCG</u> CGGGAC <u>CCGGCGGT</u> GC <u>CTCCATGGTGGTGC</u> CG	6289
		CGCGCAC <u>CCACCATGGAGAGGGACC</u> GGCCGG <u>TCCCGCGGTGC</u> GC TT <u>CCGGCTTGTGCT</u> <u>ACGGGGCGCGCTCGCTCCGGTAGTCC</u> TC <u>ATGCCGAGCGGC</u> AT <u>CTGCCGGCTCCGGG</u>	6290
		CCGCCCC <u>CGTAGCAACAA</u>	6291
20	Waxy starch GBSS <i>Triticum turgidum</i> Lys52Term AAG-TAG	TT <u>GTTGCT</u> <u>ACGGGGCGG</u>	6292

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Triticum turgidum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6293
	TGGCGCGACCACCATGGAGAGGGACCGCCGGTCCCACGGT CGCTTCCGGCTTTGTT <u>A</u> CTTCGGGGCGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGCGCATCTGCCGGCTCCG	6294
	CCCCGAAGTAACAAAGC	6295
	GCTTGTT <u>A</u> CTTCGGGG	6296
10 Waxy starch GBSS <i>Triticum turgidum</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGAAGCAATAAGCCGGAAAGCGCACCGCGGAC CCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6297
	CCGTGGCGCGACCACCATGGAGAGGGACCGCCGGTCCCACGG GTGCGCTTCCGGCTTT <u>A</u> TTGCTCAGGGCGCGCTCGCTCCGG TAGTCCTCATGCCGAGCGCGCATCTGCCGGCT	6298
	CGAAGCAATAAGCCGG	6299
	CCGGCTT <u>A</u> TTGCTCG	6300
15 Waxy starch GBSS <i>Triticum turgidum</i> Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCC CGAACAAACAAGCCGGTAAGCGCACCGCGGACCCGGCGGTG CCTCTCCATGGTGGTGCACGCCA	6301
	CGGCGCTGCCGTGGCGCGACCACCATGGAGAGGGACCGCCG GGTCCCAGGGTGCCT <u>A</u> CCGGCTTGGTGCCTCGGGCGCGC TCGCTCCGGTAGTCCTCATGCCGAGCGCGCATC	6302
	AAAGCCGGTAAGCGCAC	6303
	GTGCGCTT <u>A</u> CCGGCTT	6304
20 Waxy starch GBSS <i>Aegilops speltoides</i> Gln28Term CAG-TAG	CAGCTGCCACCTCCGCCACCGTCCTCGGCATACCGACAGGTT CCGCCATGCAGGTT <u>C</u> AGGGCGTGAAGCCCCGGAGCCGGCAG ATGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	6305
	TCGCTCCGACAGTCCTCATGCCGAGCGCGCATCTGCCGGCTC CGGGGCCTCACGCCCT <u>A</u> AAACCTGCATGGCGAACCTGTCGGT GATGCCGAGGACGGTGGCGGAGGTGGCGAGCTG	6306
	CAGGTT <u>C</u> AGGGCGTG	6307
	CACGCCCT <u>A</u> AAACCTG	6308
25 Waxy starch GBSS <i>Aegilops speltoides</i> Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAAGCCCCGGAGCCGGCAGATGCGCCGC TCGGCATGAGGACTGTC <u>T</u> GAGCGAGCGCCGCCGAAGCAACAA AGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCC	6309
	GGCACCGCCGGTCCCGCGGTGCCTTCCGGCTTGGCTTC GGGGCGGGCGCTCGCT <u>C</u> AGACAGTCCTCATGCCGAGCGCGCAT CTGCCGGCTCCGGGCTCACGCCCTGGAAACC	6310

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Aegilops speltoides</i> Lys52Term AAG-TAG	GGACTGTCT <u>GAGCGAGC</u>	6311
	GCTCGCT <u>CAGACAGTCC</u>	6312
	CCCCGGAGCCGGCAGATGCGCCGCTGGCATGAGGA <u>TGT</u> CG GAGCGAGCGCCGCCCG <u>TAGCAACAAAGCCGGAAAGCGCACCG</u> CGGGACCCGGCGGTGCCTCTCGATGGTGGTGC <u>CG</u>	6313
	CGCGCACCA <u>CCATCGAGAGG</u> CACC <u>GGCCGGG</u> TCCCGCGGTGC <u>CG</u> TTCCGGCTTGTG <u>TACGGGGCGGC</u> TCGCTCCGACAGTCC TCATGCC <u>GAGCGGCC</u> CATCTGCCGGGCTCCGGGG	6314
	CCGCCCC <u>GTAGCAACAA</u>	6315
10 Waxy starch GBSS <i>Aegilops speltoides</i> Gln53Term CAA-TAA	CGGAGCCCG <u>CAGATGCGCCG</u> CTGGCATGAGGA <u>CTGT</u> GGAG	6317
	CGAGCGCC <u>CCCCGAAG</u> <u>TAAACAAAGCCGGAAAGCGCACCGCGG</u> GACCCGGCGGTGCCTCTCGATGGTGGTGC <u>CGCGCCA</u>	
	TGGCGCG <u>ACCACCATCGAGAGG</u> CACC <u>GGCCGGG</u> TCCCGCGGTG CGCTTCCGGCTTGT <u>TACTTCGGGGCGCG</u> TCGCTCCGACAG	6318
	TCCTCATGCC <u>GAGCGGCC</u> CATCTGCCGGGCTCCG CCCCGAAG <u>TAAACAAAGC</u>	6319
	GCTTG <u>TACTTCGGGG</u>	6320
15 Waxy starch GBSS <i>Aegilops speltoides</i> Gln54Term CAA-TAA	AGCCC <u>GGCAGATGCCCG</u> CTGGCATGAGGA <u>CTGT</u> GGAGCGA GCGCC <u>GGCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGAC</u> CCGGCGGTGCCTCTCGATGGTGGTGC <u>CGCGCCACCG</u>	6321
	CGGTGGCGCG <u>UACCACCATCGAGAGG</u> CACC <u>GGCCGGG</u> TCCCGCG GTGC <u>GCTTCCGGCTTATTGCTCGGGCGCG</u> TCGCTCCGA CAGTCCTCATGCC <u>GAGCGGCC</u> CATCTGCCGGGCT	6322
	CGAAG <u>CAATAAAGCCGG</u>	6323
	CCGGCTT <u>ATTGCTTCG</u>	6324
	Waxy starch GBSS <i>Oryza glaberrima</i> Gln8Term CAG-TAG	6325 6326 6327 6328
	AGTGCAGAGAT <u>CTTCACAGCAACAGCTAGACAACCACCATGTCG</u> GCTCT <u>ACCACTCGCTAGCTGCCACCTCGGCCACCGGCTCG</u> CATCG <u>CTGACAGGTGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT</u> GCAGCGACGACGGCGCCGAC <u>CTGTCAGCGATGCCGAAGCCGGT</u> GCCCGAGGTGGCGAG <u>CTAGGACGTGGTGA</u> GAGAGCCGACATGGT GTTGT <u>CTAGCTGTTGCTGTGGAAGATCTCGCACT</u> CCACGT <u>CCTAGCTGCC</u> GGCGAG <u>CTAGGACGTGG</u>	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Oryza glaberrima</i> Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACT CCCAGCTGCCACCT <u>A</u> GGCCACCGGCTCGGCATCGCTGACAGG TCGGCGCCGTGTCGCTGCTCCGCCACGGGTT	6329
		AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCT <u>A</u> GGTGGCGAGCTGGGACGTGGTGAGA	6330
		GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	6331
		CGCCACCT <u>A</u> GGCCACCG	6332
10	Waxy starch GBSS <i>Oryza glaberrima</i> Ser22Term TCG-TAG	CGGCTCTACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGT <u>A</u> GGCGCCGTGTCGCTGCTCCGCCACGG	6333
		GTTCAGGGCCTCAAGCCCCGAGCCCCGCCGG	6334
		CCGGCGGGGCTGCAGGGGCTTGAGGCCCTGGAACCGTGGCGGA GCAGCGACGACGGCGCT <u>A</u> CCCTGTCAGCGATGCCGAAGCCGGTG	6335
		GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6336
		TGACAGGT <u>A</u> GGCGCCGT	
15	Waxy starch GBSS <i>Oryza glaberrima</i> Ser25Term TCG-TAG	CCACGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTGGCGCCGT <u>A</u> GTGCTGCTCCGCCACGGGTTCCAGG	6337
		GCCTCAAGCCCCGAGCCCCGCCGGCGACGC	6338
		CGTGGCGAGCAGCGACT <u>A</u> CCGCGCCGACCTGTCAGCGATGCC	
		GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6339
		GGCGCCGT <u>A</u> GTGCTGC	6340
20	Waxy starch GBSS <i>Oryza glaberrima</i> Ser26Term TCG-TAG	CGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTGGCGCCGTG <u>A</u> GCTGCTCCGCCACGGGTTCCAGGGCCT	6341
		CAAGCCCCGAGCCCCGCCGGCGACGCAC	6342
		GTGCGTGCCTGCCGGCGGGCTGCGGGCTTGAGGCCCTGGA ACCCGTGGCGAGCAGCT <u>A</u> CGACGGCGCCGACCTGTCAGCGATG	
		CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACCG	6343
		GCCGTCGT <u>A</u> GCTGCTCC	6344
25	Waxy starch GBSS <i>Oryza sativa</i> Gln8Term CAG-TAG	TCCACAGCAAGAGCTAACAGCCGACCGTGTGCACCACCATGTCG GCTCTCACCACT <u>A</u> GGCTGCCACCTCGGCCACCGGCTTCGG	6345
		CATCGCCGACAGGTGGCGCCGACCTGTCGGGATGCCGAAGCCGGT GCAGCGACGACGGCGCCGACCTGTCGGGATGCCGAAGCCGGT	6346
		GGCCGAGGTGGCGAGCT <u>A</u> GGACGTGGTGAGAGCCGACATGGT GTGCACACGGTCGGCTGTTAGCTTGTGGA	

	Phenotype Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Oryza sativa</i> Ser12Term TCG-TAG	CCACGTCC <u>T</u> AGCTCGCC	6347
		GGCGAGCT <u>A</u> GGACGTGG	6348
		CTAACAGCCGACCGTGTGCACCACCATGTCGGCTCTCACCACT CCCAGCTGCCAC <u>C</u> AGGCCACCGGCTCGGCATGCCGACAGG TCGGCGCCGTCGCTGCTTCGCCACGGGTT	6349
		AACCCGTGGCGAAGCAGCGACGACGGGCCGACCTGTGGCGAT GCCGAAGCCGGTGG <u>C</u> TAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTCACACGGTCGGCTGTTAG	6350
		CGCCAC <u>C</u> CTAGGCCACCG	6351
		CGGTGG <u>C</u> CTAGGTGGCG	6352
	Waxy starch GBSS <i>Oryza sativa</i> Ser22Term TCG-TAG	CGGCTCTACCACGTCCCAGCTGCCACCTCGGCCACCGGCTTC GGCATGCCGACAG <u>G</u> TAGGCGCCGTCGCTGCTGCCACGG GTTCCAGGGCCTCAAGCCCC <u>G</u> TAGCCCAGCCGG	6353
		CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAAACCCGTGGCGAA GCAGCGACGACGGGCC <u>T</u> ACCTGTGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6354
		CGACAGGT <u>A</u> GGCGCCGT	6355
		ACGGCGC <u>C</u> CTACCTGTGCG	6356
		CCACGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATGCC GACAGGTGGCGCC <u>G</u> GTAGTCGCTGCTTCGCCACGGGTTCCAGGG CCTCAAGCCCC <u>G</u> TAGCCCAGCCGGGGACGC	6357
15	Waxy starch GBSS <i>Oryza sativa</i> Ser25Term TCG-TAG	CGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAAACC CGTGGCGAAGCAG <u>G</u> ACTACGGGCCACCTGTGGCGATGCC GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6358
		GGCGCC <u>G</u> TAGTCGCTGCG	6359
		GCAGCGACTACGGGCC	6360
		CGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATGCCGAC AGGTGGCGCC <u>G</u> GTAGTCGCTGCTTCGCCACGGGTTCCAGGGCCT CAAGCCCC <u>G</u> TAGCCCAGCCGGGGACGCATC	6361
		GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA CCC <u>G</u> TGGCGAAGCAG <u>G</u> CTACGACGGGCCACCTGTGGCGATGC CGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6362
20	Waxy starch GBSS <i>Oryza sativa</i> Ser26Term TCG-TAG	GGCGTCG <u>T</u> AGCTGCTTC	6363
		GAAGCAG <u>G</u> CTACGACGGC	6364

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Hordeum vulgare</i> Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCCATGGC GGCTCTGCCACGTCTAGCTGCCACCTCCGGCACCGTCCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTC	6365
		GAAAACCTGGACGCCGAATCTGCGGTGACGCCGAGGACGGTG CCGGAGGTGGCGAGCTAGGACGTGGCCAGAGCCCACATGGCGC CGCGCACAGGGTGTGGTACCTGCAGTGAGAGAC	6366
		CCACGTCTAGCTGCC	6367
		GGCGAGCTAGGACGTGG	6368
10	Waxy starch GBSS <i>Hordeum vulgare</i> Arg21Term AGA-TGA	ATGGCGGCTCTGGCCACGTCCCAGCTGCCACCTCCGGCACCGT CCTCGGCGTCACCGACTGATTCCGGCGTCCAGGTTTCAGGGCCT CAGGCCCGGAACCCGGCGGATCGGGCGCTT	6369
		CAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAA CCTGGACGCCGGAATCAGTCGGTGACGCCGAGGACGGTGCCGG AGGTGGCGAGCTGGGACGTGGCCAGAGCCCACAT	6370
		TCACCGACTGATTCCGG	6371
		CCGGAATCAGTCGGTGA	6372
		CAGCTGCCACCTCCGGCACCGTCCTCGCGTCACCGACAGATT CCGGCGTCCAGGTTTAGGGCTCAGGCCCGGAACCCGGCGG ATGCGGCGCTTGGTATGAGGACTATCGGAGCAA	6373
15	Waxy starch GBSS <i>Hordeum vulgare</i> Gln28Term CAG-TAG	TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCC GGGGCCTGAGGCCCTAAAAACCTGGACGCCGGAATCTGCGGTG ACGCCGAGGACGGTGCCTGGAGGTGGCGAGCTG	6374
		CAGGTTTTAGGGCCTC	6375
		GAGGCCCTAAAAACCTG	6376
		GTTTCAAGGGCTCAGGCCCGGAACCCGGCGGATCGGGCGCT TGGTATGAGGACTATCTGAGCAAGCGCCGCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT	6377
20	Waxy starch GBSS <i>Hordeum vulgare</i> Gly46Term GGA-TGA	AGAGGCACCGCCGGCTCCCGCGGTGCCTTCCGGCTTGCCTC GGGGCGGCCTGCTCAGATAGTCCTCATACCAAGCGCCGCATC CGCCGGGTTCCGGGCCTGAGGCCCTGAAAACC	6378
		GGACTATCTGAGCAAGC	6379
		GCTTGCTCAGATAGTCC	6380
		CCCCGGAACCGGGCGGATGCGCGCTTGGTATGAGGACTATCGG AGCAAGCGCCGCCCGTAGCAAAGCCGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGGCGCCA	6381
25	Waxy starch GBSS <i>Hordeum vulgare</i> Lys52Term AAG-TAG	TGGCGCTCACCACCAACGGAGAGGCACGCCGGCTCCCGCGGTG CGCTTCCGGCTTGTCAAGGGCGGGCGCTTGTCTCCGATAGTCC TCATACCAAGCGCCGCATCCGCCGGTTCCGGGG	6382

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Zea mays</i> Gln8Term CAG-TAG	CCGGCCCCGT <u>AGCAAAGC</u>	6383
		GCTTGCT <u>ACGGGGCGG</u>	6384
		ACGTCTTTCTCTCTCCTACGCAGTGGATTAATCGGCATGGCGG CTCTGGCCACGTCGTAGCTCGTCGCAACCGCGCCGGCCTGGC GTCCCGGACCGTCCACGTTCCGCCGCGCG	6385
		CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCAGGCC GCGCGTTGCGACGAGCT <u>ACGACGTGGCCAGAGCCGCATGCCA</u> TTAACCACTGCGTAGGAGAGAGAGAAAAGACGT	6386
		CCACGTCG <u>TAGCTCGTC</u>	6387
		GACGAGCT <u>ACGACGTGG</u>	6388
	Waxy starch GBSS <i>Zea mays</i> Gln30Term CAG-TAG	GTCGCAACCGCGGCCGGCTGGCGTCCGGACGCGTCCACGT TCCGCCGCGGCGCCCGC <u>TAGGGCCTGAGGGGGGCCCGGGCGTC</u> GGCGCGGGCGGACACGCTCAGCATGCGGACCAGCG	6389
		CGCTGGTCGCATGCTAGCGTGTCCGCCGCCGACGCC GGCCCCCCTCAGGCC <u>TACGCGCGCCGGCGAACGTGGAC</u> GCGTCCGGGACGCCAGGCCGGCGCGTTGCGAC	6390
		GCGCCGCG <u>TAGGGCCTG</u>	6391
		CAGGCC <u>TACGCGGCCG</u>	6392
		TCCCGGACCGTCCACGTTCCGCCGCCGCCGCCAGGGCCT GAGGGGGGCCCGGGCGT <u>AGGCGGCGGGACACGCTCAGCATG</u> CGGACCACGCGCGCGCGGCCAGGCACCAGCA	6393
15	Waxy starch GBSS <i>Zea mays</i> Ser38Term TCG-TAG	TGCTGGTCCTGGCGCCGCGCGCTGGTCCGCATGCTGA GCGTGTCCGCCGCC <u>TACGCCGGGCCCCCTCAGGCCCTG</u> CGCGCGCCGCCGGCGAACGTGGACGCGTCCGGGA	6394
		CCGGGCG <u>TAGGCGGCCG</u>	6395
		CCGCCG <u>CCCTACGCCCGG</u>	6396
		GCGTCGGCGGCCGGGACACGCTCAGCATGCGGACCAGCGCGC GCGCGGCCCAAGGCA <u>CTAGCAGCAGGCCGCCGGGCA</u> GTTCGGCGCTCGCTCGTGTGCGCCAGCGCCGGCA	6397
		TGCCGGCGCTGGCGCACACGACGAGCGACGGGAAACCTGCC GCGCGGCCCTGCTGCT <u>AGTGCCTGGCGCCGCCGCGCCTG</u> GTCCGCATGCTGAGCGTGTCCGCCGCCGACGC	6398
20	Waxy starch GBSS <i>Zea mays</i> Ser57Term CAG-TAG	CCAGGC <u>ACTAGCAGCAG</u>	6399
		CTGCTGCT <u>AGTGCCTGG</u>	6400

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Zea mays</i> Gln58Term CAG-TAG	TCGGCGGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCG CGGCGCCCAGGCACCAGTAGCAGGCGCCGCCGGGGCAGGTT CCCGTCGCTCGTCGTGCGCCAGCGCCGGCATGA	6401
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGAACCTGCC CCGCGGCCGCCTGCT <u>A</u> CTGGTGCCCTGGCGCCGCCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGA	6402
	GGCACCA <u>G</u> TAGCAGGCG	6403
	CGCCTGCT <u>A</u> CTGGTGCC	6404

Example 11**Altering fatty acid content of plants**

Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearoyl- and oleoyl-ACP.

A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearoyl-acyl carrier protein (stearoyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

Table 22
Oligonucleotides to produce plants with reduced palmitate

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
25	Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser8Term TCG-TAG	TTTGGTGGCAGTGTCTTGAAACGCTTCATCTCCCTCGTCATGGTGGC CACCTCTGCTACGTAGTCATTCTTCCTGTACCATCTTCACTT GATCCTAATGGAAAAGGCAATAAGATTGG	6405
30		CCAATCTTATTGCCTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAACATGACTACGTAGCAGAGGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAAA	6406

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser9Term TCA-TGA	TGCTACGT <u>A</u> TCATTCT	6407
		AGAATGACT <u>A</u> CGTAGCA	6408
		GGTGGCAGTGTCTTGAAACGCTTCATCTCCTCGTCATGGTGGCCA CCTCTGCTACGT <u>G</u> ATTCTTCCTGTACCATCTTCACTTGAT CCTAATGGAAAAGGCAATAAGATTGGGTC	6409
		GACCAATCTTATTGCCCTTTCCATTAGGATCAAGTGAAGAAGATG GTACAGGAAAAGAAT <u>C</u> ACGACGTAGCAGAGGTGGCCACCATGACGA GGAGATGAAGCGTTCAAAGACACTGCCACC	6410
		TACGT <u>C</u> GT <u>G</u> ATTCTTC	6411
		GAAAGAAC <u>T</u> ACGACGTA	6412
	Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser17Term TCA-TGA	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGT <u>C</u> GT <u>C</u> ATTCTTC TGTACCATCTT <u>C</u> TT <u>G</u> ACTTGATCCTAATGGAAAAGGCAATAAGATT GGGTCTACGAATCTTGCTGGACTCAATT	6413
		GAATTGAGTCCAGCAAGATT <u>C</u> GTAGACCCAATCTTATTGCCCTTT CATTAGGATCAAGT <u>C</u> AAGAAGATGGTACAGGAAAGAATGACGACG TAGCAGAGGTGGCCACCATGACGAGGAGAT	6414
		ATCTTCTT <u>G</u> ACTTGATC	6415
		GATCAAGT <u>C</u> AAGAAGAT	6416
		GTGGCCACCTCTGCTACGT <u>C</u> GT <u>C</u> ATTCTTCCTGTACC <u>A</u> TCTT CACTTGATCCTAAT <u>I</u> GAAAAGGCAATAAGATTGGGTCTACGAATCT TGCTGGACTCAATTCTGCACCTA <u>A</u> CTCTG CAGAGTTAGGTGCAGAATT <u>G</u> AGTCCAGCAAGATT <u>C</u> GTAGACCCA TCTTATTGCCCTTT <u>C</u> ATTAGGATCAAGTGAAGAAGATGGTACAGG AAAGAAC <u>T</u> GACGACGTAGCAGAGGTGGCCAC	6417
10	Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Gly22Term GGA-TGA	ATCCTAATT <u>I</u> GAAAAGGC	6418
		GCC <u>T</u> TT <u>C</u> AATTAGGAT	6419
		GCTTGAATT <u>T</u> GTGATCTGATTGGTAATTGTGGCCACAATGG <u>T</u> GC TA <u>T</u> CTGCCGCCACGT <u>G</u> ATCATTCTTCCGGT <u>G</u> ACTTCCCCTCTGGG GATGCCAA <u>A</u> TCGGCAATCCCGGAAAAGG	6420
		CCTTTCCGGGATTGCCCGATTGGCATCCCCAGAACGGGAAGTC AACGGAAA <u>A</u> ATGAT <u>C</u> ACGTGGCGGCAGTAGCAACCATTGTGGCC ACAATTAA <u>C</u> CAATCAGATCACAAATTCAAGC	6421
		CGCCACGT <u>G</u> ATCATTCT	6422
15	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser8Term TCA-TGA	AGAATGAT <u>C</u> ACGTGGCG	6423
			6424
20			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser9Term TCA-TGA	TGAATTGTGATCTGATTGGTTAATTGTGCCACAATGGTGCTAC TGCCGCCACGT <u>CATGATTCTTC</u> CGTTGACTTCCCCCTCTGGGGAT GCCAAATCGGGCAATCCCGAAAAGGGTC	6425
		GACCCTTTCCGGGATTGCCGATTGGCATCCCCAGAAGGGGAA GTCAACGGAAAGAACATGACGTGGCGGAGTAGCAACCATTGTG GCCACAATTAAACCAATCAGATCACAAATTCA	6426
		CACGT <u>CATGATTCTTC</u>	6427
		GAAAGAACATGACGTG	6428
10	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Leu13Term TTG-TAG	CTGATTGGTTAATTGTGCCACAATGGTGCTACTGCCGCCACGT CATCATTCTTC <u>CGTA</u> GA <u>CTTCCCCTCTGGGGATGCCAAATCGG</u> GCAATCCCGAAAAGGGTCGGTGAGTTTGG	6429
		CCAAA <u>ACTCACCGACCC</u> TTTCCGGGATTGCCGATTGGCATCC CCAGAAGGGGAAGT <u>CTACGGAAAGAACATGATGACGTGGCGGAGT</u> AGCAACCATTGTGCCACAATTAAACCAATCAG	6430
		CTTCCGTA <u>GA</u> CTTCCC	6431
		GGGAAGT <u>CTACGGAAAG</u>	6432
		ATGGTTGCTACTGCCGCCACGT <u>CATCATTCTTC</u> CGTTGACTTCCC CTTCTGGGGATGCC <u>TA</u> ATGGCAATCCCGAAAAGGGTCGGTG AGTTTGGGT <u>CAATGAAGTCGAAATCCGCGG</u>	6433
15	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Lys21Term AAA-TAA	CCGGGGATT <u>CGACTTC</u> ATTGACCCAAACTCACCGACCC <u>TTTCC</u> GGGATTGCC <u>CGATTAGGC</u> ATCCCCAGAAGGGGAAGT <u>CAACGGAA</u> AGAACATGATGACGTGGCGGAGTAGCAACC <u>AT</u>	6434
		GGGATGCC <u>TA</u> ATGGGC	6435
		GCCCGATT <u>AGGC</u> ATCCC	6436
		GGGATT <u>CGACATGGCGTTT</u>	6437
		CCGAGCTT <u>CGTTT</u> CGAGTC <u>AGAGGAGTCAGGTGAAGAAGTG</u> ACTGGGAAAAACGCC <u>ATGT</u> CACAGCAGTAGCAACC <u>ATGGTTTTA</u> AAA <u>ACAAC</u> TTCAATT <u>CGTGTGAAATCCC</u>	6438
20	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser8Term TCG-TAG	TGTGACAT <u>AGGC</u> GT	6439
		AAA <u>ACGCC</u> T <u>ATGT</u> CACA	6440
		TGTGACAT <u>AGGC</u> GT	6441
		CCCA <u>AGTC</u> ACTT <u>CTTGAC</u> CTGACTCCTCTGACT <u>CGAAAACAAGAAG</u> CTCGGA <u>AGCAT</u> CAAG <u>TCGAAGCC</u> ATCGGT	6442
		ACCGATGGCT <u>CGACTT</u> GATGCTCCGAG <u>CTTCTGTTTCGAGT</u> CAGAGGAGTC <u>AGGT</u> CAAGAAC <u>GTGACTGGAAAACGCC</u> GATGTCA CAGCAGTAG <u>CAACC</u> ATGGTTTT <u>AAAAACA</u>	6442
25	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser16Term TCA-TGA	TGTGACAT <u>AGGC</u> GT	6441
		ACCGATGGCT <u>CGACTT</u> GATGCTCCGAG <u>CTTCTGTTTCGAGT</u> CAGAGGAGTC <u>AGGT</u> CAAGAAC <u>GTGACTGGAAAACGCC</u> GATGTCA CAGCAGTAG <u>CAACC</u> ATGGTTTT <u>AAAAACA</u>	6442

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser22Term TCG-TAG	CACTTCTT <u>GACCTGACT</u>	6443
	AGTCAGGT <u>CAAGAAGTG</u>	6444
	TTGCTACTGCTGTGACATGGCGTTTTCCCAGTCACCTTCACC TGACTCCTCTGACT <u>AGAAAAACAAGAACGATGGCTTCGACTTGATGCTCCGA</u> GAAGCCATCGGTTCTCTGGAAAGTTGCA	6445
	TGCAAACCTCCAGAAGAACCGATGGCTTCGACTTGATGCTCCGA GCTTCTTGT <u>TTCTAGTCAGAGGAGTCAGGTGAAGAAGTACTGG</u> GAAAAACGCCGATGTACAGCAGTAGCAA	6446
	CTCTGACT <u>AGAAAAACA</u>	6447
10 Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Lys23Term AAA-TAA	TGTTTTCT <u>AGTCAGAG</u>	6448
	GCTACTGCTGTGACATGGCGTTTTCCCAGTCACCTTCACCTG ACTCCTCTGACT <u>CGTAAAACAAGAACGATGGCTTCGACTTGATGCTCCGA</u> AGCCATCGGTTCTCTGGAAAGTTGCAAG	6449
	CTTGCAAACCTCCAGAAGAACCGATGGCTTCGACTTGATGCTCC GAGCTTCTTGT <u>TTACGAGTCAGAGGAGTCAGGTGAAGAAGTGCAC</u> TGGGAAAAACGCCGATGTACAGCAGTAGC	6450
	CTGACTCG <u>TTAAACAAG</u>	6451
	CTTGT <u>TTTACGAGTCAG</u>	6452
15 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Ser14Term TCG-TAG	CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTG CATTCTTCCCCGTGT <u>AGTCCCCGGTCACCTCCTAGACCAGGAA</u> AGCCCGGAAATGGGTATCGAGCTTCAGCCC	6453
	GGGCTGAAGCTCGATGACCCATTCCGGGTTCTGGTCTAGAG GAGGTGACCGGGGACT <u>ACACGGGGAAAGATGCAGAGCTTGCAGC</u> GGTAGGCCACCATTGTCTTCAACGAGCGGGAG	6454
	CCCCGTGT <u>AGTCCCCGG</u>	6455
	CCGGGGACT <u>ACACGGGG</u>	6456
	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTCCCGTGTGTCGCC CCGGTCACCTCCT <u>TGACCAAGGGAAAGCCCCGGAAATGGGTATCG</u> AGCTTCAGCCCCATCAAGCCAAATTGTGCG	6457
20 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Arg21Term AGA-TGA	CGACAAATTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTC CGGGCTTCTGGTC <u>AAGAGGAGGTGACCGGGGACGACACGGG</u> GAAGAACGAGCTTGCAGCGGTAGCCACCAT	6458
	CCTCCTCT <u>TGACCAAGGA</u>	6459
	TCCTGGT <u>CAAGAGGAGG</u>	6460

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTCCCCGTGTCGTCCCCGGTC ACCTCCTCTAGACCA <u>T</u> GAAAGCCCGGAAATGGGTATCGAGCTTC AGCCCCATCAAGCCCAAATTGTCGCCAATG	6461
		CATTGGCGACAAATTGGGCTTGATGGGCTGAAGCTCGATGACC CATTTCCGGGCTTC <u>A</u> TGGTCTAGAGGAGGTGACCGGGGACGAC	6462
		ACGGGGAAGAACATGCAGAGCTTGCAGCGTAGC CTAGACCA <u>T</u> GAAAGCCC	6463
		GGGCTTCA <u>T</u> GGTCTAG	6464
10	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTCCCCGTGTCGTCCCCGGTCACC TCCTCTAGACCA <u>T</u> GAGCCGGAAATGGGTATCGAGCTTCAGC CCCATCAAGCCCAAATTGTCGCCAATGGCG	6465
		CGCCATTGGCGACAAATTGGGCTTGATGGGCTGAAGCTCGATG ACCCATTCCGGGCT <u>A</u> TCCTGGTCTAGAGGAGGTGACCGGGGAC GACACGGGGAAGAACATGCAGAGCTTGCAGCGGT	6466
		GACCAGGA <u>T</u> AGCCCGGA	6467
		TCGGGCT <u>A</u> TCCTGGTC	6468
		GCCACCGCTGCAAGTTCTGCATTCTCCCCCTGCCGTCCCCGGAC ACCTCCTCTAGGCCG <u>T</u> GAAAGCTCGGAATGGGTATCGAGCTTG AGCCCCCTCAAGCCCAAATTGTCGCCAATG	6469
15	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly23Term GGA-TGA	CATTGGCGACAAATTGGGCTTGAGGGGGCTCAAGCTCGATGACC CATTTCCGAGCTTC <u>A</u> CGGCCTAGAGGAGGTGTCGGGGACGGC AGGGGGAAGAACATGCAGAACTTGCAGCGGTGGC	6470
		CTAGGCCG <u>T</u> GAAAGCTC	6471
		GAGCTTCA <u>C</u> GGCCTAG	6472
		ACCGCTGCAAGTTCTGCATTCTCCCCCTGCCGTCCCCGGACACC TCCTCTAGGCCGGG <u>A</u> TGCTCGGAATGGGTATCGAGCTTGAGC CCCCTCAAGCCCAAATTGTCGCCAATGCCG	6473
		CGGCATTGGCGACAAATTGGGCTTGAGGGGGCTCAAGCTCGAT GACCCATTCCGAGCT <u>A</u> TCCCGGCCTAGAGGAGGTGTCGGGGGA CGGCAGGGGGAAAGAACATGCAGAACTTGCAGCGGT	6474
20	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Lys24Term AAG-TAG	GGCCGGG <u>A</u> TGCTCGGA	6475
		TCGGAGCT <u>A</u> CCCAGGCC	6476
		GCAAGTTCTGCATTCTCCCCCTGCCGTCCCCGGACACCTCCTCT AGGCCGGGAAAGCT <u>T</u> GAAATGGGTATCGAGCTTGAGCCCCCT CAAGCCCAAATTGTCGCCAATGCCGGGTGA	6477
		TCAACCCGGCATTGGCGACAAATTGGGCTTGAGGGGGCTCAAGC TCGATGACCCATT <u>C</u> AGAGCTTCCGGCCTAGAGGAGGTGTCGG GGGACGGCAGGGGGAAAGAACATGCAGAACTTGC	6478

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Ser29Term TCA-TGA	GAAAGCT <u>T</u> GAAATGGG	6479
		CCCATT <u>T</u> CAGAGCTTC	6480
		CATTCTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGAA AGCTCGGAAATGGGTGATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGTTGAAGGTTAAGGC	6481
		GCCTTAACCTCAACCCGGCATTGGCGACAAATTGGGCTTGAGG GGGCTCAAGCTCGAT <u>C</u> ACCCATTCCGAGCTTCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGAAGAATG	6482
		AAATGGGT <u>G</u> ATCGAGCT	6483
		AGCTCGAT <u>C</u> ACCCATT	6484
	Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Ser9Term TCG-TAG	CGTTTAAGTGGATGGACATTAAAGTGTAAATCATGGTAGCTAT GAGTGCTACTGCGT <u>A</u> GCTGTTCCGGTTCTCCAAAACCTCA CTCTGGAGCCAAGACATCTGATAAGCTTG	6485
		CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTGGGAA GAAACCGGAAACAGCTACGCAGTAGCACTCATAGCTACCATGATT AAAACACTAAATGTCGATCCACTAAACG	6486
		TACTGCGT <u>A</u> GCTGTT	6487
		GAAACAGCTACGCAGTA	6488
		AGTGTAAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTC CGGTTTCTCCCC <u>A</u> ACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTGCTG	6489
10	Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys17Term AAA-TAA	CAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGT <u>A</u> TGGGAAGAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAACACT	6490
		CTTCCCC <u>A</u> ACCTCAC	6491
		GTGAGGTT <u>A</u> TGGGAAG	6492
		ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTCCGGTTCTCCC CAAAACCTCACTCT <u>G</u> AGCCAAGACATCTGATAAGCTTGAGGTGA ACCAGGTAGTGTGCTGTGCGCGGAATCA	6493
		TGATTCCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATC AGATGTCTGGCT <u>C</u> AAGAGTGAGGTTGGGAAGAACCGGAAA CAGCGACCGCAGTAGCACTCATAGCTACCAT	6494
15	Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Gly21Term GGA-TGA	CTCACTCT <u>G</u> AGCCAAG	6495
		CTTGGCT <u>A</u> AGAGTGAG	6496

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys23Term AAG-TAG	GCTATGAGTGCTACTCGCTCGCTGTTCCGGTTCTCCCCAAAC CTCACTCTGGAGCCTAGACATCTGATAAGCTGGAGGTGAACCAG GTAGTGTGCTGTGCCGGAATCAAGACAA	6497
		TTGTCTTATTCCGCGCACAGCAACACTACCTGGTCACCTCCAAG CTTATCAGATGTCTAGGCTCCAGAGTGAGGTTTGGGAAGAAC CGGAAACAGCGACGCAGTAGCACTCATAGC	6498
		CTGGAGCCTAGACATCT	6499
		AGATGTCTAGGCTCCAG	6500
10	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTCTGCATGCTCCCTGTTCCATCC CCAGGAGCCTCCCCTAACCTGGGAAGTTAGGCAACTGGTCATCG AGTTTGGCCCTTGAAGGCCAAGTCAA	6501
		TTGACTTGGGCTTCAAGGAAGGGCTAAACTCGATGACCAGTTGC CTAACTTCCCAGGTTAAGGGGAGGCTCTGGGATGGAACAGGG AAGCATGCAGAACTTGCTGCAGCAGCCACCAT	6502
		CCTCCCCTAACCTGGG	6503
		CCCAGGTTAAGGGGAGG	6504
		GCTGCAGCAAGTTCTGCATGCTCCCTGTTCCATCCCCAGGAGCC TCCCCTAACCTGGGTAGTTAGGCAACTGGTCATCGAGTTGAGC CCTTGAAGGCCAAGTCAATCCCCAATG	6505
15	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys24Term AAG-TAG	CATTGGGATTGACTTGGGCTTCAAGGAAGGGCTAAACTCGATG ACCAGTTGCCTAACTACCCAGGTTAGGGGAGGCTCTGGGATG GAACAGGGAAAGCATGCAGAACTTGCTGCAGC	6506
		AACCTGGGTAGTTAGGC	6507
		GCCTAACTACCCAGGTT	6508
		TGCATGCTCCCTGTTCCATCCCCAGGAGCCTCCCCTAACCTGG GAAGTTAGGCAACTGATCATCGAGTTGAGCCCTTGAAGCC CAAGTCATCCCCAATGGCGGATTTCAGGTT	6509
20	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Trp28Term TGG-TGA	AACCTGAAATCCGCCATTGGGATTGACTTGGGCTTCAAGGAAGG GCTCAAACTCGATGATCAGTTGCCTAACTTCCCAGGTTAGGGGA GGCTCCTGGGATGGAACAGGGAAAGCATGCA	6510
		GGCAACTGATCATCGAG	6511
		CTCGATGATCAGTTGCC	6512
		CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAACCTGGGA AGTTAGGCAACTGGTGTATCGAGTTGAGCCCTTGAAGCCCA AGTCATCCCCAATGGCGGATTTCAGGTTAA	6513
25	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Ser29Term TCA-TGA	TTAACCTGAAATCCGCCATTGGGATTGACTTGGGCTTCAAGGAA GGGCTCAAACTCGATCACCAGTTGCCTAACTTCCCAGGTTAGGG GAGGCTCCTGGGATGGAACAGGGAAAGCATG	6514

	Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys21Term AAA-TAA	CAACTGGT <u>GATCGAGTT</u>	6515
		AACTCGAT <u>CACCAGTTG</u>	6516
		ATGGTGGCTGCCGAGCAAGTCTGCATTCTCCGTCCAACC CCGGGAATCTCCCCT <u>TAAACCCGGGAAGTCGGTAATGGTGGCTT</u> CAGGTTAAGGCAAACGCCAATGCCCATCCTA	6517
		TAGGATGGGCATTGGCGTTGCCTTAACCTGAAAGGCCACCATTAC CGAACCTCCC <u>GGGTTAAGGGAGATTCCC</u> GGGGTTGGAACGGAG AAGAATGCAGAACTTGCTGCCGCAGCCACCAT	6518
		TCTCCC <u>CTTAAACCCGGG</u>	6519
10	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	CCCGGG <u>TTAAGGGGAGA</u>	6520
		GCCGCAGCAAGTTCTGCATTCTCCGTCCAACCCC <u>GGGAATC</u> TCCCCTAAACCC <u>GGG</u> <u>TAGTT</u> CGGTAA <u>TGGTGGCTT</u> CAGGTTAAG GCAAACGCCAATGCCCATCCTAGTCTAAAGT	6521
		ACTTAGACTAGGATGGGCATTGGCGTTGCCTTAACCTGAAAGCC ACCATTACCGAA <u>CTACCCGGGTTAAGGGAGATTCCC</u> GGGGTTGG AACGGAGAAGAAC <u>TGCTGCCGC</u>	6522
		AACCCGGG <u>TAGTT</u> CGGT	6523
		ACCGAA <u>CTACCCGGGTT</u>	6524
15	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gln31Term CAG-TAG	TTCTCCGTCCAACCCC <u>GGGAATCTCCCCTAAACCCGGGAAGTTC</u> GGTAATGGTGGCTT <u>TAGGT</u> TAAGGCAAACGCCAATGCCCATCCT AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	6525
		CTTCAGTCTCGAGGC <u>GTGCCAGACTTTAGACTAGGATGGCATTGG</u> CGTTTGCCTTAAC <u>CTAAAAGCCACCATTACCGAACTTCCC</u> GGGGTT AGGGGAGATTCCC <u>GGGGTTGGAACGGAGAA</u>	6526
		GTGGCTT <u>TTAGGT</u> TAAG	6527
		CTTAAC <u>CTAAAAGCCAC</u>	6528
		GTTCCAACCCC <u>GGGAATCTCCCCTAAACCCGGGAAGTTC</u> GGTAAT GGTGGCTT <u>CAGGTT</u> AGGCAAACGCCAATGCCCATCCTAGTCTA AAGTCTGGCAGCCTCGAGACTGAAGATGACA	6529
20	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys33Term AAG-TAG	TGTCA <u>TCTCAGTCTCGAGGC</u> GTGCCAGACTTAGACTAGGATGGG CATTGGCGTTGCCT <u>AAACCTGAAAGCCACCATTACCGAACTCCC</u> GGGTTAGGGAGATTCCC <u>GGGGTTGGAAC</u>	6530
		TTCAGGTT <u>TTAGGCAAAC</u>	6531
		GTTTGCC <u>TTAAACCTGAA</u>	6532

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Gln21Term CAA-TAA	ATGTTGAAGCTCTGTATAATGCGACTGATAAGTTACAGACCCCTCTCTCGCATTCTCATTAACCGGATCCGGCACACCCGGAGAACCGTCTCCTCGGTCATCTGAGGAAAC	6533
		GTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGTGTGCCGGATCCGGTTAATGAGAATGCGAGAAGAGGGTCTGTAACATTACAGAGCTCAACAT	6534
		ATTCTCATTAACCGGAT	6535
		ATCCGGTTAATGAGAAT	6536
10	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Arg28Term AGA-TGA	GCGACTGATAAGTTACAGACCCCTTTCTCGCATTCTCATCAACCGGATCCGGCACACCCGGTGAACCGTCTCCTCCGTGTGCTCTCATCTGAGGAAACCGGTTCTCGA	6537
		CTCGCAAAGGATCGAGAACCGGTTCTCGATCCTTGCGAG	6538
		CGGAGGAGACGGTTACCCGGTGTGCCGGATCCGGTTGATGAGAA	
		TGCGAGAAGAGGGTCTGTAACCTATCAGTCGC	
		CACACCGGTGAACCGTC	6539
15	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Ser24Term TCG-TAG	CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCCGGAGAA	6541
		CCGTCTCCTCCGTGTAGTGTCTCATCTGAGGAAACCGGTTCTCGATCCTTGCGAGCGATCGTATCTGCTGATCA	
		TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTC	6542
		CTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTGCG	
		CGGATCCGGTTGATGAGAATGCGAGAAGAGGG	
20	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Cys25Term TGC-TGA	CTCCGTGTAGTGTCTC	6543
		GAGAGCACTACACGGAG	6544
		CTTCTCGCATTCTCATCAACCGGATCCGGCACACCCGGAGAACCGT	6545
		CTCCCTCCGTGTGATCTCATCTGAGGAAACCGGTTCTCGATCC	
		TTTGCAGCGATCGTATCTGCTGATCAAGGA	
25	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG	6546
		TTTCCTCAGATGAGATCACGACACGGAGGAGACGGTTCTCCGGTG	
		TGCCGGATCCGGTTGATGAGAATGCGAGAAG	
		GTGTCGTGATCTCATCT	6547
		AGATGAGATCACGACAC	6548
	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG	ATTCCTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAGG	6549
		GCATAAAAATGTAAGAGCTTCGTATAATGTGACTAACAACTTAC	
		ACACCTTCTCCTTCTCCGATTCTC	
		GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTAGTCACA	6550
		TTACACGAAAGCTTACATTGATGCCCTTTTTTTATGGTC	
		CTGAGGTTGGTTATAGAAGAAGAAT	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAATGT <u>A</u> GAAGCTTT	6551
	AAAGCTT <u>C</u> TACATTTT	6552
5 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Lys3Term AAG-TAG	TCTTCTTCTATAACCAAAACCTCAGGAACCATAAAAAAAAAGGG CATCAAAATGTT <u>G</u> AGCTTCGTGAATGTGACTAACAACTTACAC ACCTTCTCCTCTCGATTCCCTCCC GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGAAGTTGTTAGTCA CATTACACGAAAGCT <u>A</u> CAACATTGGATGCCCTTTTTATGG TTCCTGAGGTTGGTTATAGAAGAAGA AAATGTT <u>G</u> AGCTTCG	6553 6554 6555 6556
10 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Ser5Term TCG-TAG	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAGGGCATCAA AATGTTGAAGCTT <u>A</u> GTGAATGTGACTAACAACTTACACACCTCT CCTCTTCTCGATTCCCTCCCTTTCAT ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGAAGTTG TTAGTCACATTACACT <u>A</u> AGCTCAACATTGGATGCCCTTTTT TTATGGTTCCCTGAGGTTGGTTATAG GAAGCTT <u>A</u> GTGAATG CATTACACT <u>A</u> AGCTTC	6557 6558 6559 6560
15 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Cys6Term TGT-TGA	AAACCAAAACCTCAGGAACCATAAAAAAAAAGGGCATAAAAATG TTGAAGCTTCGTGA <u>A</u> ATGTGACTAACAACTTACACACCTCTCCT CTTCTCCGATTCCCTCCCTTTCATCCCG CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGA AGTTGTTAGTCACATT <u>C</u> ACGAAAGCTCAACATTGGATGCCCT TTTTTTATGGTTCCCTGAGGTTGGTT CTTCGT <u>G</u> AAATGTGAC GTCACATT <u>C</u> ACGAAAG	6561 6562 6563 6564

Table 23
Oligonucleotides to produce plants with increased stearate

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGGATTCAATTATCATATC CAGAAATGGCTCTATAGTTAACCCCTTGGTGGCATCTCAGCCTTA CAAATCCCTTCCTCGACTCGTCCGCCAA	6565
10		TTGGCGGACGAGTCGAGGAAGGGATTGTAGGCTGAGATGCCA CCAAGGGTTAAACTATAGAGCCATTCTGGATATGATGAATGAAT CCTCTTTCTACAGAGCTAGAGCTCTCCC	6566
		TGGCTCTATAGTTAAC	6567
		GTTAAACTATAGAGCCA	6568
15	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGGATTCAATTATCCAGAAATGGCTCT AAAGTTAACCCCTTAGGTGGCATCTCAGCCTTACAATTCCCTTCC TCGACTCGTCCGCCAACCTCCTCTTCAG	6569
		CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGATTGTAA GGCTGAGATGCCACCTAACGGTTAAACTTAGAGCCATTCTGGAT ATGATGAATGAATCCTCTTCTACAGAG	6570
		TAACCCTTAGTGGCAT	6571
		ATGCCACCTAACGGTTA	6572
20	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Gln12Term CAG-TAG	AGAAGGATTCAATTATCCAGAAATGGCTCTAAAGTTAAC CTTGGTGGCATCTTACCTAACATTCCCTCCTCGACTCGTCC GCCAACTCCTCTTCAGATCTCCCAAGT	6573
		ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA GGGAATTGTAGGCTAACATGCCACCAAGGGTTAAACTTAGAG CCATTCTGGATATGATGAATGAATCCTCT	6574
		TGGCATCTAGCCTTAC	6575
		GTAAGGCTAACATGCCA	6576
25	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Phe14Term TAC-TAG	TCATTCAATCCAGAAATGGCTCTAAAGTTAACCCCTTGGTG GCATCTCAGCCTTAAATTCCCTCCTCGACTCGTCCGCCAAC CTTCTTCAGATCTCCCAAGTCTCTGC	6577
		GCAGAGGAACCTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG TCGAGGAAGGGATTCTAAGGCTGAGATGCCACCAAGGGTTAA ACTTCTAGAGCCATTCTGGATATGATGAATGA	6578
		CAGCCTTAAATTCCC	6579
		GGGAATTCTAAGGCTG	6580

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAA AAAGAAAATGGCAT <u>A</u> GAAGCTAACCCCTTGGCATCTCAGCCTAAC AAACTCCCTCCTCGGCTCGTCCGCCAAT	6581
		ATTGGCGGACGAGCCGAGGAAGGGAGTTGTAAGGCTGAGATGC CAAAGGGTTAACGCTT <u>C</u> TATGCCATTTCCTTTTGATACGAGGTT TGATGTTCTTCAGACACGAGCGAGCTCTC	6582
		AATGGCAT <u>A</u> GAAGCTTA	6583
		TAAGCTT <u>C</u> TATGCCATT	6584
10	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAA AGAAAATGGCATT <u>G</u> TAGCTAACCCCTTGGCATCTCAGCCTACAA ACTCCCTCCTCGGCTCGTCCGCCAATCT	6585
		AGATTGGCGGACGAGCCGAGGAAGGGAGTTGTAAGGCTGAGAT GCCAAAGGGTTAACGCT <u>A</u> CAATGCCATTTCCTTTTGATACGAG GTTTGATGTTCTTCAGACACGAGCGAGCTC	6586
		TGGCATTG <u>T</u> AGCTTAAC	6587
		GTAAAGCT <u>A</u> CAATGCCA	6588
		TCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATT GAAGCTTAACCC <u>T</u> AGGCATCTCAGCCTACAAACTCCCTCCTCG GCTCGTCCGCCAATCTCTACTCTCAGATC	6589
15	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu8Term TTG-TAG	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTT GTAAGGCTGAGATGCC <u>T</u> AGGGTTAACGCTTCAATGCCATTTCCTT TTTTGATACGAGGTTGATGTTCTTCAGA	6590
		TAACCCT <u>T</u> AGGCATCTC	6591
		GAGATGCC <u>T</u> AGGGTTA	6592
		AACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATT <u>G</u> AAGCTTAA CCCTTGGCAT <u>T</u> AGCCTTACAAACTCCCTCCTCGGCTCGTCCG CCAATCTCTACTCTCAGATCTCCCAGT	6593
		ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA GGGAGTTGTAAGGCT <u>A</u> AGATGCCAAAGGGTTAACGCTTCAATGCC ATTTCTTTTGATACGAGGTTGATGTT	6594
20	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Gln11Term CAG-TAG	TGGCAT <u>T</u> AGCCTTAC	6595
		GTAAGGCT <u>A</u> AGATGCCA	6596
		AACCAAAAGAAAAAGGTAAAGAAAAAAACAATGGCTCTCAAGCTCA ATCCCTTCCCTT <u>C</u> TAAACCCAAAAGTTACCTTCTCGCTCTCCA CCAATGGCCAGTACCAAGATCTCCTAAGT	6597
		ACTTAGGAGATCTGGTACTGGCATTGGTGGAAAGAGCGAAAGAAG GTAACCTTGGGTT <u>A</u> AGAAAGGAAAGGATTGAGCTGAGAGCCAT TGTTTTTTCTTACCTTTCTTTGGTT	6598
25	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln27Term CAA-TAA		
30	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln27Term CAA-TAA		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln29Term CAA-TAA	TCCTTTCT <u>TAAACCCAA</u>	6599
		TTGGGT <u>TTAAGAAAGGA</u>	6600
		AAGAAAAAGGT <u>AAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTT</u> TCCTTTCT <u>CAAACCTAAAGTTACCTCTTCGCTCTCCACCAATG</u> GCCAGTACC <u>AGATCTCTTAAGTTCTACA</u>	6601
		TGTAGAAC <u>TTAGGAGATCTGGTACTGGCCATTGGTGGAGAGCGA</u> AAGAAGGT <u>AACTTTAGGTTGAGAAAGGAAAGGATTGAGCTTGAG</u> AGCCATT <u>GTTTTTTCTTACCTTTCTT</u>	6602
		CTCAAAC <u>CTAAAGTTA</u>	6603
		TAAC <u>TTTAGGTTGAG</u>	6604
	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys30Term AAG-TAG	AAAAAGGT <u>AAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTCC</u> TTTCT <u>CAAACCCAATAGTTACCTCTTCGCTCTCCACCAATGGC</u> CAGTACC <u>AGATCTCTTAAGTTCTACATGG</u>	6605
		CCATGT <u>AGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAGAG</u> CGAAAGAAG <u>GTAACTATTGGTTGAGAAAGGAAAGGATTGAGCT</u> TGAGAG <u>CCATTGTTTTTTCTTACCTTTT</u>	6606
		AAACCC <u>AAATAGTTACCT</u>	6607
		AGGT <u>AACTATTGGGTTT</u>	6608
		TCTCAAAC <u>CCAAAAGTTACCTCTTCGCTCTCCACCAATGCCA</u> GTACC <u>CAGATCTCCTTAGTTCTACATGGCCTCTACCCCTCAAGTCTGG</u> TTCT <u>TAAGGAAGTTGAGAATCTCAAGAACG</u>	6609
15	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys46Term AAG-TAG	GCT <u>CTTGAGATTCTCAACTTCTTAGAACCAAGACTTGAGGGTAGA</u> GGCC <u>ATGTAGAACTAAGGAGATCTGGTACTGGCATTGGTGGAG</u> AGCG <u>AAAGAAGGTAACTTTGGTTGAGA</u>	6610
		GAT <u>CTCCTTAGTTCTAC</u>	6611
		GTAG <u>AACTAAGGAGATC</u>	6612
		TCT <u>CTGATTCAATTAACTTACTCATCAATGGCTCTGAGACTGAA</u> CCCT <u>ATCCCCACCTAAACCTTCCCTCCCCAAATGCCAGTCT</u> CAG <u>ATCTCCCAGGTTCCGCATGCCCTCTA</u>	6613
		TAGAG <u>GGCCATGCCAACCTGGGAGATCTGAGACTGGCATTGG</u> GGG <u>AGGGAGAAGGTTAGGTGGGATAGGGTTCAGTCTCAGAGC</u> CATT <u>GATGAGTAAAGATTAAATGAATCAGAAGA</u>	6614
20	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln11Term CAA-TAA	TCCC <u>CCACCTAAACCTTC</u>	6615
		GAAG <u>GGTTAGGTGGGA</u>	6616

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligo	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln17Term CAA-TAA	CTTTACTCATCAATGGCTCTGAGACTGAACCCATCCCCACCCAAA CCTTCTCCCTCCCCAAATGGCCAGTCTCAGATCTCCAGGTTC GCATGGCCTCTACCCTCCGCTCCGGTTCCA	6617
		TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGAT CTGAGACTGGCCATTAGGGGAGGGAGAAGGTTGGTGGGAT AGGGTTCACTCTCAGAGCCATTGATGAGTAAAG	6618
		CCCTCCCCAAATGGCC	6619
		GGCCATTAGGGAGGG	6620
10	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Arg22Term AGA-TGA	GCTCTGAGACTGAACCCATCCCCACCCAAACCTTCTCCCTCCCC CAAATGGCCAGTCTCTGATCTCCAGGTTCGCATGGCCTCTACC CTCCGCTCCGGTTCCAAGAGAGGTGAAAATA	6621
		TATTTCAACCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGC GGAACCTGGGAGATCAGAGACTGGCCATTGGGGGAGGGAGAAG GTTTGGGTGGGGATAGGGTTCACTCTCAGAGC	6622
		CCAGTCTCTGATCTCCC	6623
		GGGAGATCAGAGACTGG	6624
15	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Lys37Term AAA-TAA	CAAATGGCCAGTCTCAGATCTCCAGGTTCGCATGGCCTCTACC CTCCGCTCCGGTTCTAACAGAGGTGAAATATTAAGAACCCATTCA CTCCTCCCAGAGAACGTGCATGTTCAAGTAA	6625
		TTACTGAACATGCACTCTCTGGGAGGAGTGAATGGCTCTTAAT ATTTCAACCTCTTAAAGAACCGGAGCGGAGGGTAGAGGCCATGCG GAACCTGGGAGATGTGAGACTGGCCATTG	6626
		CCGGTTCTAACAGAGGT	6627
		AACCTCTTAAAGAACCGG	6628
20	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	CAACAAAGCACACACAAGAACACATCAACAAATGGCGATTGCATCA ATACGGCGACGTTTAATCAGACCTGTACCGTTATTGCCTTCC TCAACCGAAACCTCTCAGATCTCCCAAAT	6629
		ATTTGGGAGATCTGAGAGGTTGGTTGAGGAACCGCAATGAAC GGTACAGGTCTGATTAAACGTGCCGTATTGATGCGAATGCCA TTGTTGATGTTCTGTGTGCTTGTG	6630
		CGACGTTTAATCAGAC	6631
		GTCTGATTAAACGTG	6632
25	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser12Term TCA-TGA	AAGCACACACAAGAACACATCAACAAATGGCGATTGCATCAATAC GGCGACGTTCAATGAGACCTGTACCGTTATTGCCTTCCCAA CCGAAACCTCTCAGATCTCCCAAATCGC	6633
		GCGAATTGGGAGATCTGAGAGGTTGGTTGAGGAACCGCAAT GAACGGTACAGGTCTCATTGAAACGTGCCGTATTGATGCGAATC	6634
		GCCATTGTTGATGTTGTTCTGTGTGCTT	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAC-TAG	GTTTCAAT <u>GAGACCTGT</u>	6635
		ACAGGTCT <u>ATTGAAAC</u>	6636
		AAGAACAA <u>CATCAACAATGGCGATTCGCATCAATACGGCGACGTT</u> CAATCAGAC <u>CTGTAGCGTCATT</u> CGCGTTCCCTAACCGAAACCTC	6637
		TCAGATCTCCAA <u>ATTGCCATGGCTTC</u>	
		GGAAGCC <u>CATGGCGAATTGGGAGATCTGAGAGGTT</u> CGGTTGAGG AAACGCGAAT <u>GAACGCTACAGGTCTGATTGAAACGTCGCCGTATT</u> GATGCGAATGCCATTGTTGATGTTGTTCTT	6638
		<u>GACCTGTAGCGTT</u> CATT	6639
		AATGAAC <u>GCTACAGGT</u> C	6640
	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser17Term TCA-TGA	CAACATCAACAA <u>TGGCGATTCGCATCAATACGGCGACGTTCAATC</u> AGACCTGT <u>ACCGTTGATT</u> CGCGTTCCCTAACCGAAACCTCTCAGA	6641
		TCTCCAA <u>ATTGCCATGGCTTCACCAT</u>	
		ATGGTGG <u>AAGCCATGGCGAATTGGGAGATCTGAGAGGTT</u> CGGT TGAGGAAACGCGAAT <u>CAACGGTACAGGTCTGATTGAAACGTCGCC</u> GTATTGATGCGAATGCCATTGTTGATGTTG	6642
		<u>GTACCGTTGATT</u> CGCGT	6643
		ACGCGAAT <u>CAACGGTAC</u>	6644
10	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Arg4Term CGA-TGA	ACACACAA <u>CACACACTCAATCACACACATCATCATCTTCTTCATC</u> AACGATGGCGCTT <u>I</u> GAATGAGTCCGGTGACGCTTCAACGGGAGAT	6645
		ATATCCTTCATA <u>CACTTTCATCAATCGA</u>	
		TCGATTGAT <u>AAAAGTGTATGAGGATATAT</u> CTCCGTTGAAGCGT	6646
		CACCGGACTCATT <u>CAAAGGCCATCGT</u> GATGAAGAAGATGATGA	
		TGTGTGTGATT <u>GAGTGTGTGTGT</u>	
15	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	<u>TGGCGCTT</u> I <u>GAATGAGT</u>	6647
		ACTCATT <u>CAAAGGCCA</u>	6648
		ACACACACATCATCATCTTCTTCATCAACGATGGCGCTT <u>CGAATGA</u>	
		GTCCGGTGACGCTT <u>I</u> ACGGGAGATATATCCTTCATA <u>CACTTTCA</u>	
		TCAATCGAAA <u>ATCTCAGATCTCCTAAAT</u>	
20	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	ATTTAGGAGATCTGAGAT <u>TTTCGATTGATGAAAGTGTATGAAGG</u>	6649
		ATATATCTCCCGTT <u>AAAGCGTCACCGGACTCATT</u> CGAAGCGCCAT	6650
		CGTTGATGAAGAAGATGATGATGTTGTGTGT	
		<u>TGACGCTT</u> I <u>ACGGGAG</u>	6651
		CTCCCGTT <u>AAAGCGTCA</u>	6652

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGG TGACGCTTCAACGGTAGATATATCCTTCATACACTTTCATCAATCG AAAAATCTCAGATCTCCTAAATTGCGGA	6653
		TCGCGAATTAGGAGATCTGAGATTTTCGATTGATGAAAAGTGT TGAAGGATATATCT <u>ACCGTTGAAGCGTCACCGGACTCATTGAA</u> G CGCCATCGTTGATGAAGAAGATGATGATGT	6654
		TTCAACGGTAGATATAT	6655
		ATATATCT <u>ACCGTTGAA</u>	6656
10	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAT-TAG	ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTACGCTT CAACGGGAGATATA <u>G</u> CCTTCATACACTTTCATCAATCGAAAATCT CAGATCTCCTAAATTGCGATGGCTTCC	6657
		GGAAGCCATCGCAATTAGGAGATCTGAGATTTTCGATTGATGA AAAGTGTATGAAGG <u>C</u> TATATCTCCCGTTGAAGCGTCACCGGACTC ATTGAAGGCCATCGTTGATGAAGAAGAT	6658
		GAGATATA <u>G</u> CCTTCATA	6659
		TATGAAGG <u>C</u> TATATCTC	6660
		AACTCAGCCAGCTGCCCAAAACAACAGCGCAGAAAAACCTICA ACAACAATGGCTCT <u>C</u> TAGCTCAACCCAGTCACCACCTCCCTCAA CACGCTCCCTCAACA <u>A</u> CTTCTCCTCCAGAT	6661
15	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys4Term AAG-TAG	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTGAAGGGAAAGGTG GTGACTGGGTTGAGCT <u>A</u> GAGAGCCATTGTTGTTGAAGGTTTCTG CGCTGTTTTGGGGCAAGCTGGCTGAGTT	6662
		TGGCTCT <u>C</u> TAGCTAAC	6663
		GTTGAGCT <u>A</u> GAGAGCCA	6664
		GGCGAGAAAAACCTCAACAACAATGGCTCTCAAGCTCAACCCAG TCACCACCTCCCTT <u>G</u> AACACGCTCCCTCAACA <u>A</u> CTTCTCCTCCAG ATCTCCTCGCACCTTCTCATGGCTGCTT	6665
20	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Ser13Term TCA-TGA	GAAGCAGCCATGAGAAAGGTGCAGGGAGATCTGGAGGAGAAGTT GTTGAGGGAGCGTGT <u>C</u> AAGGGAAAGGTGGTACTGGGTTGAGCT TGAGAGCCATTGTTGTTGAAGGTTTCTGCGC	6666
		CTTCCCTT <u>G</u> AACACGCT	6667
		AGCGTGT <u>T</u> CAAGGGAAAG	6668
		CTCAAGCTCAACCCAGTCACCACCTCCCTCAACACGCTCCCTC AACAA <u>C</u> TTCTCCT <u>C</u> TGATCTCCTCGCACCTTCTCATGGCTGCTT CCACTTCAATTCCACCTCCACCAAGTAAG	6669
25	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Arg23Term AGA-TGA	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAAGCAGCCATGAGAA AGGTGCGAGGGAGAT <u>C</u> AGGAGGAGAAGTTGTTGAGGGAGCGTGT	6670
		GAAGGGAAAGTGGTACTGGGTTGAGCTTGAG	
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys41Term AAG-TAG	TCTCCTCC <u>T</u> GATCTCCT	6671
		AGGAGATCAGGAGGAGA	6672
		TCCTCCAGATCTCCTCGCACCTTCTCATGGCTGCTTCACTTTCA ATTCCACCTCCACCT <u>A</u> GATCTCCTCCCTCGGAATCTCCG CCGATTTC <u>T</u> TAAGCGATTGATCGTAGA	6673
		TCTACGATCAATCGCTAAAAGAAATCGGCCGAGATTCCGAGGAG GAGGAGATGCTTACT <u>A</u> GGTGGAGGTGGAATTGAAAGTGGAAAGCAG CCATGAGAAAGGTGCGAGGAGATCTGGAGGA	6674
		CCTCCACCT <u>A</u> GTAAGCA	6675
		TGCTTACT <u>A</u> GGTGGAGG	6676
	Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Arg21Term AGA-TGA	ATGGCACTGAAACTTTGCTTTCCACCCCCACAAGATGCCTCCCTCC CCGATGCTCGTAT <u>T</u> GATCTCACAGGGTTTCATGGCTTCAACTAT TCATTCTCCTCTATGGAGGTGGAAAG	6677
		CTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCTGTGAGAT <u>C</u> A <u>G</u> A <u>T</u> ACGAGCATGGGAAGGAAGGCATCTT GTGGGGTGGAAAGCAAAGTTCA <u>G</u> ATGCCAT	6678
		CTCGTAT <u>T</u> GATCTCAC	6679
		GTGAGAT <u>C</u> A <u>G</u> A <u>T</u> ACGAG	6680
		CCCACAAGATGCCTCCCTCCCCGATGCTCGTATCAGATCTCAC GGGTTTCATGGCTT <u>G</u> A <u>U</u> CTATTCTCCTCTATGGAGGTGG AAAAGTTAAAAGCCTTCACGCCCTCCACG	6681
10	Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Ser29Term TCA-TGA	CGTGGAGGC <u>G</u> TGAAAGGTTTAA <u>C</u> TTCCGACCTCCATAGAAG GAGAATGAATAGTTCAAGCCATGAAACCC <u>T</u> GTGAGATCTGATACG AGCATGGGGAAAGGAAGGCATCTTG <u>GG</u>	6682
		CATGGCTT <u>G</u> A <u>U</u> CTATT <u>C</u>	6683
		GAATAGTT <u>C</u> A <u>U</u> CCATG	6684
		GATGCTCGTATCAGATCTCACAGGGTTTCATGGCTTCAACTATT <u>C</u> ATTCTCCTCTATG <u>T</u> AGGTGGAAA <u>G</u> TAAAAGCCTTCACGCC TCCACGAGAGGTACATGTTCAAGTAACCC	6685
		GGGTTACTGAACATGTACCTCTCGTGGAGGC <u>G</u> TGAAAGGCTTTT AACTTTCCGACCT <u>A</u> CA <u>T</u> AGAAGGAGAATGAATAGTTGAAGCCATG AAAACCC <u>T</u> GTGAGATCTGATACGAGC <u>T</u> AC	6686
15	Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Glu37Term GAG-TAG	CTTCTATG <u>T</u> AGGTGG <u>GA</u> TCCGACCT <u>A</u> CA <u>T</u> AGAAG	6687 6688

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTCATGGCTCAACTATTCTCTC CTTCTATGGAGGTCT <u>GAAAAGTTAAAAGCCTTCACGCCTCCACG</u> AGAGGTACATGTTCAAGTAACCCATTCTC	6689
		AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTCAAAG GCTTTTA <u>ACTTTCA</u> GACCTCCATAGAAGGAGAATGAATAGTTGA AGCCATGAAAACCCTGTGAGATCTGATACG	6690
		TGGAGGTCT <u>GAAAAGTT</u>	6691
		AACTTT <u>CA</u> GACCTCCA	6692
10	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys4Term AAA-TAA	TTCTCGTTTGTCGCCCCCTTGCTCTCTCTATCAGGCACG GAGAAATGGCACT <u>GTA</u> ACTCAGTCCAGTCATGTTCAATCTCAGAA GCTCCATTCTGCTCCTATCCGCC	6693
		AAGGCGGATAGGAGGCAAGAAATGGAAGCTCTGAGATTGAAACA TGACTGGACTGAGTT <u>ACAGTGCC</u> ATTCTCCGTGCCTGATAGAGA GAGAGAGCAGAGGGGACGACAAAAACGAGAA	6694
		TGGCACT <u>GTA</u> ACTCAGT	6695
		ACTGAGTT <u>ACAGTGCC</u> A	6696
		CTGCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTC AGTCCAGTCATGTT <u>TAATCTCAGAAGCTCC</u> ATTCTGCCTCCTA TCCGCC	6697
15	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln11Term CAA-TAA	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT GGAAGCTCTGAGATT <u>AAAACATGACTGGACTGAGTT</u> CAGTGCCA TTTCTCCGTGCCTGATAGAGAGAGAGCAG	6698
		TCATGTT <u>TAATCTCAG</u>	6699
		CTGAGATT <u>AAAACATGA</u>	6700
		TCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA GTCATGTT <u>CAATCT</u> <u>TAGAAGCTCC</u> ATTCTGCCTCCTATCCGC CTTCC	6701
		TGAAAACCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA GAAATGGAAGCT <u>CTAAGATTGAAACATGACTGGACTGAGTT</u> CAG TGCCATTCTCCGTGCCTGATAGAGAGAGA	6702
20	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln13Term CAG-TAG	TTCAAT <u>CTTAGAAGCTT</u>	6703
		AAGCT <u>CTAAGATTGAA</u>	6704
		CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC ATGTT <u>CAATCTCAGT</u> <u>AGCTTCC</u> ATTCTGCCTCCTATCCGCC CAATCTCAGATCTCCGAGGGTTTCATGG	6705
25	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys14Term AAG-TAG	CCATGAAAACCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGG CAAGAAATGGAAG <u>CTACTGAGATTGAAACATGACTGGACTGAGTT</u>	6706
		CAGTGCCATTCTCCGTGCCTGATAGAGAG	
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Tyr12Term TAC-TAG	AATCTCAG <u>T</u> AGCTTCCA	6707
		TGGAAG <u>C</u> TACTGAGATT	6708
		CCCCGAGATCTCGCTGCCGTCGTCATGGCGTCGCCGTCCC ACACCGCATGCCGT <u>A</u> GTCCCTGCCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCGAAGATGGTGGCCATGGCC	6709
		GGCCATGGCCACCATCTCGACATCCCATTGCTCCTCTGC CACGCCGCGCAGGACTACGGCGATGCCGTGGGACGCCCG AACGCCATGAGCAGCGGCAGCGAGATCTCGGGG	6710
		TCGCCGT <u>A</u> GTCCCTGCCG	6711
		CCGCAGG <u>A</u> CTACGGCGA	6712
	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Gln19Term CAG-TAG	CTGCTCATGGCGTTCGCCGTCCCACACCGCATGCCGTACTC CTGCCGGCGTGGCG <u>T</u> AGAGGAGGAGCAATGGGATGTCGAAGA TGGTGGCCATGCCCTCCACCATCACAGGGTC	6713
		TGACCTGTTGATGGTGGAGGCCATGCCACCATCTCGACATCC CATTGCTCCTCT <u>T</u> ACGCCACGCCGCCAGGAGTACGGCGAT GCCGTGTGGGACGCCGAAACGCCATGAGCAG	6714
		GCGTGGCG <u>T</u> AGAGGAGG	6715
		CCTCCT <u>T</u> ACGCCACGC	6716
		CCCACACCGCATGCCGTACTCCTGCCGGCGTGGCGCAGAG GAGGAGCAATGGGATG <u>T</u> AGAAGATGGTGGCCATGCCCTCCACCA TCAACAGGGTCAAGACTGCTAAGAACGCCCTACAC	6717
10	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Ser26Term TCG-TAG	GTGTAGGGCTTCTAGCAGTCTTGACCCCTGTTGATGGTGGAGGCC ATGGCCACCATCT <u>T</u> ACATCCCATTGCTCCTCTGCCACG CCGCCGCAAGGAGTACGGCGATGCCGTGGG	6718
		TGGGATG <u>T</u> AGAAGATGG	6719
		CCATCT <u>T</u> ACATCCC	6720
		CACACCGCATGCCGTACTCCTGCCGGCGTGGCGCAGAGGAG GAGCAATGGGATG <u>T</u> CGTAGATGGTGGCCATGCCCTCCACCATCAA CAGGGTCAAGACTGCTAAGAACGCCCTACACTC	6721
		GAGTGTAGGGCTTCTAGCAGTCTTGACCCCTGTTGATGGTGGAGG CCATGGCCACCAT <u>T</u> ACGACATCCCATTGCTCCTCTGCCCA GCCGCCGCCAGGAGTACGGCGATGCCGTGG	6722
15	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Lys27Term AAG-TAG	GGATGTCG <u>T</u> AGATGGTG	6723
		CACCAT <u>T</u> ACGACATCC	6724

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Leu3Term TTG-TAG	TTCTCTCTAGGTGAGCGGGTACCAACAGAACACTAGGAGA GAGAAGCAATGGCGTAGAAGCTCACCAACACGGCCTCAATCCTT CCATGGCGGTACCTCTCGGGACTTCCTCG	6725
		CGAGGAAGTCCCAGAGAGTAACGCCATGAAAGGATTGAAGGC CGTGTGGTGAAGCTCTACGCCATTGCTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTAACCTAGAGAGAGAA	6726
		AATGGCGTAGAAGCTTC	6727
		GAAGCTTCTACGCCATT	6728
10	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Lys4Term AAG-TAG	CTCTCTCTAGGTGAGCGGGTACCAACAGAACACTAGGAGAGA GAAGCAATGGCGTTAGCTTACCCACACGGCCTCAATCCTCC ATGGCGGTACCTCTCGGGACTTCCTCGAT	6729
		ATCGAGGAAGTCCCAGAGAGTAACGCCATGAAAGGATTGAAG GCCGTGTGGTGAAGCTACAACGCCATTGCTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTAACCTAGAGAGAG	6730
		TGGCGTTAGCTTCAC	6731
		GTGAAGCTACAACGCCA	6732
15	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Ser19Term TCG-TAG	AAGCAATGGCGTTGAAGCTTACCCACACGGCCTCAATCCTCC GGCGGTTACCTCTTACGGACTCCTCGATCGTATCACCTCAGATC TCACCGCGTTTCATGGCTCTTACAAT	6733
		ATTGTAGAAGAACCATGAAAACCGGGTGGAGATCTGAGGTGATAC GATCGAGGAAGTCCCTAAAGAGGTAAACGCCATGAAAGGATTGAAG GCCGTGTGGTGAAGCTCAACGCCATTGCTT	6734
		TACCTCTTACGGACTTC	6735
		GAAGTCCCTAAAGAGGTAA	6736
20	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Gly20Term GGA-TGA	GCAATGGCGTTGAAGCTTACCCACACGGCCTCAATCCTCC GC GGTTACCTCTTCTGAGACTCCTCGATCGTATCACCTCAGATCTC ACCGCGTTTCATGGCTTCTTACAATTG	6737
		CAATTGTAGAAGAACCATGAAAACCGGGTGGAGATCTGAGGTGAT ACGATCGAGGAAGTCACGAAGAGGTAAACGCCATGAAAGGATTGA AGGCCGTGTGGTGAAGCTCAACGCCATTGCTT	6738
		CCTCTCGTAGCTTCCT	6739
		AGGAAGTCACGAAGAGG	6740
25	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Ser21Term TCA-TGA	TGGCTCTGAATCTCAACCCGGTCCACACCATTAGTGTGTC ATTGCCGTCTTCTGACCTCGTCAAACGCCCTCTCGCAGATCTCCC AAATTCTCATGGCTCCACTCTCAGCAG	6741
		CTGCTGAGAGTGGAGGCCATGAAGAATTGGGAGATCTGCGAGAA GGCGTTGACGAGGTCAAGAAAGACGGCAATCGACGACACTGAAAT GGTGTGGAAACGGGGTTGAGATTAGAGCCA	6742
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		GTCTTTCT <u>GACCTCGTC</u>	6743
		GACGAGGT <u>CAGAAAGAC</u>	6744
5	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Gln24Term CAA-TAA	AATCTCAACCCGTTCCACACCATT <u>CAGTGTGTCGATTGCCGT</u> CTTTCTCACCTCG <u>TAAACGCCTCTCGCAGATCTCCAAATTCTT</u> CATGGCTTCACTCTCAGCAGCT <u>CTTCTC</u>	6745
		GAGAAGAGCTGCTGAGAGTGGAA <u>GCCATGAAGAATTGGGAGATC</u> TGCGAGAAGGC <u>GTTAACGAGGTGAGAAAGACGGCAATCGACGA</u> CACTGAA <u>ATGGTGTGGAAACGGGTTGAGATT</u>	6746
		CACCTCG <u>TAAACGCCT</u>	6747
		AGGCG <u>TTAACGAGGTG</u>	6748
		TCCACACCATT <u>CAGTGTGTCGATTGCCGT</u> CTTCTCACCTCGTC AAACGCCTTCTCG <u>GATCTCCAAATTCTT</u> CATGGCTTCACTCT CAGCAGCTTCTC <u>CCAAGGAAGCGGAAA</u>	6749
10	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Arg29Term AGA-TGA	TTTCCGCTCCT <u>TAGGAGAAGAGCTGCTGAGAGTGGAAAGCCATGA</u> AGAATT <u>TTGGGAGATCAGCGAGAAGCGTTGACGAGGTGAGAAAG</u> ACGGCAATCGACGACACTGAA <u>ATGGTGTGGA</u>	6750
		CTTCTCG <u>GCTGATCTCCC</u>	6751
		GGGAGAT <u>CGCGAGAAG</u>	6752
		TTTCAGTGTGTCGATTGCCGT <u>CTTCTCACCTCGTCAAACGCCTT</u> CTCGCAGAT <u>CTCCCTAAATTCTT</u> CATGGCTTCACTCTCAGCAGCTC TTCTC <u>TAAGGAAGCGGAAAGCCTGAAGA</u>	6753
		TCTTCAGGCTTCCGCT <u>CCCTTAGGAGAAGAGCTGCTGAGAGTGG</u> AAGCCAT <u>GAAGAATTAGGGAGATCTGCAGAAGGC</u> TTGACGAG GTGAGAAAGACGGCAATCGACGACACTGAAA	6754
15	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Lys32Term AAA-TAA	GAT <u>CTCCCTAAATTCTT</u> C	6755
		GAAGAATT <u>AGGGAGATC</u>	6756
		AAATAGTC <u>GAGGTGAAAAACAGAGCATCAACAATGGCACTGAATA</u> CAATGGGGTGT <u>CGTAAAATCTCACAAATGTTACCATTTCTTGT</u> TCTTCAG <u>CCAGATCTGAGCGAGTTT</u> CAT	6757
		ATGAAA <u>ACTCGCTCAGATCTGGCTGAAGAACACAAGGAAATGGTAACA</u> TTTG <u>TGAGATTT</u> CACGACACCCATTGATATT <u>CAGTGCCATTGTT</u> GATGCT <u>CTGTTT</u> CACCTCGACTATTT	6758
		GGTGT <u>CGTAAAATCTC</u>	6759
20	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu10Term TTA-TGA	GAG <u>ATTT</u> CACGACACC	6760

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCA ATGGGGTGTGTTATAATCTCACAAATGTTACCATTCCCTTGTCT TCAGCCAGATCTGAGCGAGTTTCATGG	6761
		CCATGAAAACTCGCTCAGATCTGGCTGAAGAACAGGAAATGGTA ACATTTTGAGATTATAACGACACCCCATTGATATTCACTGCCATT GTTGATGCTCTGTTTACCTCGACTAT	6762
		TGTCGTTATAATCTCAC	6763
		GTGAGATTATAACGACA	6764
10	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys14Term AAA-TAA	GTGAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGTGT CGTTAAAATCTCACTAAATGTTACCATTCCCTTGTCTTCAGCCAGA TCTGAGCGAGTTTCATGGCTTCACCA	6765
		TGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAG GAAATGGTAACATTAGTGAGATTAAACGACACCCCATTGATATT AGTGCCATTGTTGATGCTCTGTTTAC	6766
		AATCTCACTAAATGTTA	6767
		TAACATTAGTGAGATT	6768
15	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu16Term TTA-TGA	ACAGAGCATCAACAATGGCACTGAATATCAATGGGTGTGTTAAA ATCTCACAAATGTGACCATTCCCTTGTCTTCAGCCAGATCTGAG CGAGTTTCATGGCTTCACCAATTCTCG	6769
		CGATGAATGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAA GAACAAGGAAATGGT CAC ATTGAGATTAAACGACACCCCATT TGATATTCACTGCCATTGTTGATGCTCTGT	6770
		CAAATGT G ACCAATTTC	6771
		GAAATGGT C ACATTTC	6772
20	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser21Term TCA-TGA	TGGCTCTGAGGCTGAACCCCTAACCCCTCACAGAAGCTTTCTCTC TCCCTCTTCATCAT G ATCTCTCTTCATCGTTCTCGCTTC AAATGGCTAGCCTCAGATCTCCAAGGTT	6773
		AACCTTGGAGATCTGAGGCTAGCCATTGAGGAAGCGAGAACGAT GAAGAAGAAGAAGAT C ATGATGAAGAAGGAGAGAGAAAGAGCTTC TGTGAAGGGTTAGGGTTAGCCTCAGAGCCA	6774
		TTCATCAT G ATCTCTT	6775
		AAGAAGAT C ATGATGAA	6776
25	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser26Term TCA-TGA	ACCCTAACCTTCACAGAAGCTTTCTCTCCTTCTCATCATCA TCTTCTTCTTCTT G ATCGTTCTCGCTTCCTCAAATGGCTAGCCTCA GATCTCCAAGGTTCCGCATGGCCTCCAC	6777
		GTGGAGGCCATGCGAACCTGGAGATCTGAGGCTAGCCATTGA GGAAGCGAGAACGAT C AGAAGAAGAAGATGATGATGAAGAAGGA	6778
30		GAGAGAAAGAGCTCTGTGAAGGGTTAGGGT	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser27Term TCG-TAG	TTCTTCTTGATCGTTCT	6779
		AGAACGATCAAGAAGAA	6780
		CTAACCCCTCACAGAACGCTTTCTCTCCTCTCATCATCATCT TCTTCTTCTTCATA <u>G</u> TTCGCTCCTCAAATGGCTAGCCTCAGAT CTCCAAGGTCCGCATGGCCTCCACCCT	6781
		AGGGTGGAGGCCATCGGAACCTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAAC <u>T</u> ATGAAGAAGAAGATGATGATGAAGA AGGAGAGAGAAAGAGCTCTGTGAAGGGTAG	6782
		TTCTTCATA <u>G</u> TTCTCGC	6783
		GCGAGAAC <u>T</u> ATGAAGAA	6784
10	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser29Term TCG-TAG	CTTCACAGAACGCTTTCTCTCCTCTCATCATCATCATCTTCT TCTTCATCGTTCT <u>A</u> GCTTCTCAAATGGCTAGCCTCAGATCTCAA GGTCCGCATGGCCTCCACCCTCCGCAC	6785
		GTGCGGAGGGTGGAGGCCATCGGAACCTGGAGATCTGAGGCT AGCCATTGAGGAAG <u>C</u> TAAGACGATGAAGAAGAAGATGATGA TGAAGAAGGAGAGAGAAAGAGCTCTGTGAAG	6786
		ATCGTTCT <u>A</u> GCTTCTC	6787
		GAGGAAG <u>C</u> TAAGACGAT	6788
		AAAGTTAAAAGCCGTCCAAAACCCAAACCCAGGAAAGGCCAACGAA AAGAAAAAATGGCT <u>A</u> GAATTAA <u>T</u> ATGCCATGCCCTCGAAATCTCA GAAGCTCCCTGCTTGCTCTCCACCAA	6789
15	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Leu3Term TTG-TAG	TTGGTGGAAAGAGCAAAGCAAGGGAGCTCTGAGATTGAGGCG ATGGCATTAAAATT <u>C</u> TAAGCCATT <u>T</u> TTCTTGCCTTGCTTCCCT GGTTGGGTTTGACGGCTTTAAC <u>TT</u>	6790
		AATGGCT <u>A</u> GAATT <u>TT</u> A	6791
		TAAAATT <u>C</u> TAAGCCATT	6792
		CCCAAACCAAGGAAAGGCCAACGAAAAGAAAAATGGCTTGAA <u>TT</u> TAATGCCATGCC <u>A</u> GAATCTCAGAACGCTCCCTGCTTGCTCTT CCACCAAAGGCCACCC <u>T</u> AGATCTCCCAA	6793
		TTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAAAGCAAGG GAGCTTCTGAGATT <u>C</u> TAGGCATGGCATTAA <u>A</u> TTCAAAGCCATT TTTCTTCTGCTTGCC <u>T</u> TCCTGGTTGG	6794
20	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Ser1-Term TCG-TAG	CATGCC <u>A</u> GAATCTC	6795
		GAGATTCTAGGCATG	6796

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Lys11Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTGAATTAA ATGCCATCGCCTCGTAATCTCAGAACGCTCCCTGCTTTGCTCTCC ACCAAAGGCCACCCCTAGATCTCCAAGT	6797
		ACTTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAAAGCAAG GGAGCTCTGAGATTACGAGGCCATGGCATTAAAATTCAAAGCCA TTTTTCTTCGTTGCCTTCTGGTTTG	6798
		TCGCCTCGTAATCTCAG	6799
		CTGAGATTACGAGGCCA	6800
10	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Gln13Term CAG-TAG	AGGAAAGGCCAACGAAAAGAAAAAATGGCTTGAATTAAATGCCA TCGCCTCGAAATCTTAGAACGCTCCCTGCTTTGCTCTCCACCAA GGCCACCCCTAGATCTCCAAGTTTCCA	6801
		TGGAAAACCTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAA AGCAAGGGAGCTCTAAGATTTCGAGGCCATGGCATTAAAATTCAA AGCCATTTCGTTGCCTTCT	6802
		CGAAATCTAGAACGCTC	6803
		GAGCTTCTAAGATTTCG	6804

Table 24
Oligonucleotides to produce plants with reduced linolenic acid

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTCTCTTCTGGGAAGAGGC TCCAATGGCGAGCTAGGTTTATCAGAATGTGGTTAGACCTCTC CCCAGATTCTACCCCTAACACACAACACCTC	6805
10		GAGGGTTGTGTAGGGTAGAATCTGGGGAGAGGTCTAAACCA CATTCTGATAAAACCTAGCTGCCATTGGAGCCTCTCCCAAGAAG AAAAGAGGAAAAAGTCTGTGTTCTATT	6806
		GGCGAGCTGGTTTAT	6807
		ATAAAACCAAGCTCGCC	6808
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Leu6Term TTA-TGA	ACGACAGAGACTTTCTCTTCTGGGAAGAGGTCCAAT GGCGAGCTCGGTTTATCAGAATGTGGTTAGACCTCTCCCCAG ATTCTACCCCTAACACACAACACCTCTTTGC	6809
		GCAAAAGAGGTTGTGTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGATCAAACCGAGCTGCCATTGGAGCCTTCC CAAGAAGAAAAAGAGGAAAAAGTCTCTGTGCGT	6810
		CTCGGTTTATGATCAGAAT	6811
		ATTCTGATCAAACCGAG	6812
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser7Term TCA-TGA	ACAGAGACTTTCTCTTCTGGGAAGAGGTCCAATGGC GAGCTCGGTTTATGAGAATGTGGTTAGACCTCTCCCCAGATT TACCCCTAACACACAACACCTCTTTGCCTC	6813
		GAGGCAAAAGAGGTTGTGTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCTCATAAAACCGAGCTGCCATTGGAGCCTCTT CCCAAGAAGAAAAAGAGGAAAAAGTCTCTGT	6814
		GGTTTATGAGAATGTG	6815
		CACATTCTCATAAAACC	6816
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Glu8Term GAA-TAA	AGAGACTTTCTCTTCTGGGAAGAGGTCCAATGGCGA GCTCGGTTTATCATATGTGGTTAGACCTCTCCCCAGATTCTA CCCTAACACACAACACCTCTTTGCCTCTA	6817
		TAGAGGCAAAAGAGGTTGTGTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATTATGATAAAACCGAGCTGCCATTGGAGCCTC TTCCCAAGAAGAAAAAGAGGAAAAAGTCTCT	6818
		TTTTATCATATGTGGT	6819
		ACCACATTATGATAAAA	6820

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu4Term TTG-TAG	TCATCATCTCTCTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACT <u>AGGTCTTATCCGAATGTGGCATAAGACCTCTCCCAGAATCTACACCACACCCAGATCCAC</u>	6821
		GTGGATCTGGGTGTGGTAGATTCTGGGGAGAGAGGTCTTATGCCATTTCGCGATAGAGCTCTTGCTCTCTCCCCAGAAGAAGAAGATGATGA	6822
		GGCGA <u>ACTAGGTCTTAT</u>	6823
		ATAAGACCT <u>AGTTGCC</u>	6824
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu6Term TTA-TGA	TCTCTTCTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAA <u>TGGCGAACTTGGTCTGATCCGAATGTGGCATAAGACCTCTCCCCGAATCTACACCACACCCAGATCCACTTTCCCT</u>	6825
		AGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGGAGAGGTCTTATGCCACATT <u>CGGATCAGACCAAGTTGCCATTGCTAGAGCTCTTGTCTCTCTCTCCCCAGAAGAAGAAGA</u>	6826
		CTTGGTCT <u>GATCCGAAT</u>	6827
		ATTCGGAT <u>CAGACCAAG</u>	6828
		TTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTGGTCTTAT <u>CCAATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCCTCTCCA</u>	6829
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Glu8Term GAA-TAA	TGGAGAGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGGAGAGGTCTTATGCCACATT <u>AGGATAAGACCAAGTTGCCATTGCTAGAGCTCTTGTCTCTCTCCCCAGAAGAA</u>	6830
		TCTTAT <u>CCAATGTGGC</u>	6831
		GCCACATT <u>AGGATAAGA</u>	6832
		CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGA <u>ACTTGGTCTTATCCGAATGAGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCCTCTCCAACACCC</u>	6833
		GGTGTGGAGAGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGAGAGGTCTTATGCC <u>CATTGGATAAGACCAAGTTGCCATTGCTAGAGCTCTTGTCTCTCTCTCCCCAG</u>	6834
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Cys9Term TGT-TGA	TCCGAAT <u>GAGGCATAAG</u>	6835
		CTTATGCC <u>CATTGGAA</u>	6836
		ATAACAGAATT <u>GCTGAATTCTGCATTTAGCTTCTGGGTTTCAA</u>	6837
		TGGCTGCTGGTT <u>GAGTATTATCAGAATGTGGTTAAGGCCTCTCCCAGAATCTACTCACGACCCAGAATTGGT</u>	
		ACCAATTCTGGGT <u>CGTAGAGATTCTGGGAGAGGCCTAAACCACATTCTGATAATACTCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATT</u> CAGCAATTCTGTTAT	6838
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Trp5Term TGG-TGA		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Leu7Term TTA-TGA	GCTGGTT <u>GAGT</u> TATTATC	6839
		GATAATA <u>CTCAACCAGC</u>	6840
		AGAATTGCTGAATTCTGCATTTAGCTTCTGGGTTTCATGGCT GCTGGTTGGGTATT <u>GATCAGAATGTGGTTAAGGCCTCTCCCAAGA</u> ATCTACTCACGACCCAGAATTGGTTTAC	6841
		GTAAAACCAATTCTGGGTCGTGAGTAGATTCTGGGAGAGGCCTT AAACCACATTCTGAT <u>CATACCCAACCAGCAGCCATTGAAAACCCAG</u>	6842
		AAGCTAAAATGCAAGAATT <u>CAGCAATTCT</u>	
		TTGGGTAT <u>GATCAGAAT</u>	6843
		ATTCTGAT <u>CATACCCA</u>	6844
	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Ser8Term TCA-TGA	ATTGCTGAATTCTGCATTTAGCTTCTGGGTTTCATGGCTGCT GGTTGGGTATTAT <u>GAGAATGTGGTTAAGGCCTCTCCCAAGAATCT</u> ACTCACGACCCAGAATTGGTTTACATC	6845
		GATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTGGGAGAGGC CTTAAACCACATT <u>CTCATATAATACCCAACCAGCAGCCATTGAAAACC</u>	6846
		CAGAAGCTAAAATGCAAGAATT <u>CAGCAAT</u>	
		GGTATTAT <u>GAGAATGTG</u>	6847
		CACATT <u>CTCATATAACC</u>	6848
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Glu9Term GAA-TAA	TGCTGAATTCTGCATTTAGCTTCTGGGTTTCATGGCTGCTG GTTGGGTATTAT <u>CATAATGTGGTTAAGGCCTCTCCCAAGAATCTA</u> CTCACGACCCAGAATTGGTTTACATCGA	6849
		TCGATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTGGGAGAG GCCTTAAACCACATT <u>ATGATAATACCCAACCAGCAGCCATTGAAAA</u>	6850
		CCCAGAAGCTAAAATGCAAGAATT <u>CAGCA</u>	
		TATTAT <u>CTATAATGTGGT</u>	6851
		ACCACATT <u>ATGATAATA</u>	6852
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg22Term AGA-TGA	GCAAGTTGGGTTTATCAGAATGTGGCTTAGACCACTCCCAAGAA TCTACCCCTAACGCCCTGA <u>ACTGGGGCAGCCACTTCTGCCTCCTCTC</u> ACATTAAGTGAGAATT <u>TCACGTACAGATC</u>	6853
		GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGGAGGCAGAAGT. GGCTGCCCCAGTT <u>CAAGGGCTTAGGGTAGATTCTGGGAGTGGTCT</u>	6854
		AAGACCACATT <u>CTGATAAAACCCAAC</u> TTGC	
		CTAAGCCC <u>TGA</u> CTGGG	6855
		CCCAGTT <u>CA</u> GGGCTTAG	6856

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Lys34Term AAG-TAG	CTCCAAGAACCTACCCCTAACGCCAGAACTGGGGCAGCCACTTCT GCCTCCTCTCACATT <u>TAGTTGAGAATTCACGTACAGATCTGAGTG</u> GTTCTGCAATTCTTGTCTAATACTAATA	6857
		TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG TGAAATTCTCAACTAAATGTGAGAGGAGGCAGAAGTGGCTCCCC AGTTCTGGGCTTAGGGTAGATTCTGGGAG	6858
		CTCACATT <u>TAGTTGAGA</u>	6859
		TCTCAACT <u>AAATGTGAG</u>	6860
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Leu35Term TTG-TAG	CAAGAACCTACCCCTAACGCCAGAACTGGGGCAGCCACTTCTGCCT CCTCTCACATTAAAGTAGAGAATTCACGTACAGATCTGAGTGGTTC TGCAATTCTTGTCTAATACTAATAAAGA	6861
		TCTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT ACGTGAAATTCT <u>CACACTTAATGTGAGAGGAGGCAGAAGTGGCTGC</u> CCCAGTTCTGGGCTTAGGGTAGATTCTG	6862
		CATTAAGT <u>AGAGAATT</u>	6863
		AAATTCT <u>CACACTTAATG</u>	6864
		AGAACCTACCCCTAACGCCAGAACTGGGGCAGCCACTTCTGCCTCC TCTCACATTAAAG <u>TGTGAATT</u> CACGTACAGATCTGAGTGGTCTG CAATTCTTGTCTAATACTAATAAAGAGA	6865
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg36Term AGA-TGA	TCTCTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT GTACGTGAAATT <u>CACACTTAATGTGAGAGGAGGCAGAAGTGGCT</u> GCCCGAGTTCTGGGCTTAGGGTAGATTCT	6866
		TTAAGTT <u>TGTGAATTCA</u>	6867
		TGAAATT <u>CACACTTA</u> A	6868
		GCGAGTTGGGTTTATCAGAAC <u>GTGGCTGAGGCCACTCCGAGG</u> GTCTATCCTAAC <u>GCCATGA</u> ACTGGCCACCC <u>TTGTGAATTCCAATC</u> CCACAAAG <u>CTGAGATTTC</u> AAAGAACAGATC	6869
		GATCTGTTCTGAAAAT <u>CTCAGCTTGTGGATTGGAAATTCAACAA</u> AGGGTGGCCAG <u>TTCATGGCTAGGATAGACCCTGGGAGTGGCC</u> TCAGACCACATT <u>CTGATAAAACCAACTCGC</u>	6870
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Arg22Term AGA-TGA	CTAAC <u>GCCATGA</u> ACTGGC	6871
		GCCAGTT <u>CATGGCTTAG</u>	6872
		CAGAAC <u>ATGTGGCTGAGGCCACTCCGAGGGTCTATCCTAACCAA</u> GAAC <u>TTGGCCACCC</u> TT <u>AGTTGAATTCCAATCCCACAAAGCTGAGATT</u> TTCAAGAACAGAT <u>CTTGGAAATGGTCTTC</u>	6873
		GAAGAAC <u>CCATTCCAAGATCTGTTCTGAAAATCTCAGCTTG</u> GATTGGAA <u>TTCAACTAAGGGTGGCCAGTTCTGGCTTAGGATAGA</u> CCCTCGGGAG <u>GTGGCTCAGACCACATTCT</u>	6874
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG		
30	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG		

	Phenotype Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu28Term TTG-TAG	CCACCCTT <u>A</u> GTTGAATT	6875
		AATTCAACT <u>A</u> AGGGTGG	6876
		AATGTGGCTTGAGGCCACTCCCGAGGGTCTATCCTAACGCCAAGAA CTGGCCACCCCTTGT <u>A</u> GAATTCCAATCCCACAAAGCTGAGATTTCAAGAACAGATCTTGGCTTCATT	6877
		AATGAAGAACCATTTCCAAGATCTGTTCTGAAAATCTCAGCTTGT GGGATTGGAATTCTACAAAGGGTGGCCAGTTCTGGCTTAGGATA GACCCTCGGGAGTGGCCTCAGACCACATT	6878
		CCCTTTGT <u>A</u> GAATTCCA	6879
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Lys34Term AAG-TAG	TGGAATTCT <u>A</u> CAAAGGG	6880
		CTCCCGAGGGTCTATCCTAACGCCAAGAACCTGGCCACCCCTTGTG AATTCCAATCCCACAT <u>A</u> GCTGAGATTTCAAGAACAGATCTTGGAA ATGGTTCTTCATTCTGTTGTGAGTGGGA	6881
		TCCCACTCGACAAACAGAACATGAAGAACCATTTCCAAGATCTGTTCT TGAAAATCTCAGCT <u>A</u> TGTGGATTGGAATTCAACAAAGGGTGGCC AGTTCTGGCTTAGGATAGACCCCTGGGAG	6882
		ATCCCACAT <u>A</u> GCTGAGA	6883
		TCTCAGCT <u>A</u> TGTGGGAT	6884
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Tyr3Term TAC-TAG	CATCAGAGCGCGATACCTAACGCATTGCTGGGTTAAGAACATCCATG GAAGTCTATGAGTTAGGTCGTCAAGAGAGCTAGCCATCGTGTTCGC ACTAGCTGCTGGAGCTGCTTACCTAACAAAT	6885
		ATTGTTGAGGTAAAGCAGCTCCACGAGCTAGTGCAGAACACGATGGC TAGCTCTCTGACGAC <u>C</u> TAACTCATAGACTCCATGGATTCTAACCC CAGCAATGCTTAGGTATGCCGCTCTGATG	6886
		ATGAGTT <u>A</u> GGTCGTCA	6887
		CTGACGAC <u>C</u> TAACTCAT	6888
		CGGGCGATACCTAACGCATTGCTGGGTTAAGAACATCCATGGAAAGTCT ATGAGTTACGTCGT <u>C</u> TGAGAGCTAGCCATCGTGTTCGCACTAGCT GCTGGAGCTGCTTACCTAACAAATTGGCTTG	6889
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Arg6Term AGA-TGA	CAAGCCAATTGTTGAGGTAAAGCAGCTCCACGAGCTAGTGCAGAAC CGATGGCTAGCTCTCAGACGACGCTAACTCATAGACTCCATGGAT TCTTAACCCAGCAATGCTTAGGTATGCCGC	6890
		ACGTCGT <u>C</u> TGAGAGCTA	6891
		TAGCTCT <u>C</u> AGACGACGT	6892

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Glu7Term GAG-TAG	GCGATACCTAAGCATTGCTGGGTTAAGAACATGGAAGTCTATGA GTTACGTCTCAGATAGCTAGGCCATCGTGTGCACTAGCTGCTG GAGCTGCTTACCTAACAAATTGGCTTGT TCGTCAGATAGCTAGCC	6893
		AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGC ACACGATGGCTAGCTATCTGACGACGTAACCATAGACTCCATG GATTCTAACCCAGCAATGCTTAGGTATCGC	6894
		GGCTAGCTATCTGACGA	6895
			6896
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Gly17Term GGA-TGA	TCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGT TTCGCACTAGCTGCTTGAGCTGCTTACCTAACAAATTGGCTTGT GGCCTCTCTATTGGATTGCTCAAGGAACCA	6897
		TGGTTCCTTGAGCAATCCAATAGAGAGGCCAACAGCCAATTGTT GAGGTAAGCAGCTCAAGCAGCTAGTGCGAACACGATGGCTAGCT CTCTGACGACGTAACCATAGACTCCATGG	6898
		TAGCTGCTTGAGCTGCT	6899
		AGCAGCTCAAGCAGCTA	6900
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg22Term AGA-TGA	GCAAGTTGGGTTCTATCAGAACATGTTAGACCCTACCAAGAA TATACCCCAAGCCCTGAATAGGGTCTTCTCGTTGCGCCACCAA TTAAATCTGAGAAGAATTACCTTCACCTTCAC	6901
		GTGAAGGTGAAATTCTCTCAGATTAAATTGGTGGCGAACCGGA AGAAGACCCCTATTCAAGGGCTTGGGTATATTCTGGTAGTGGCTA AGACCACATTCTGATAGAACCCAACTTGC	6902
		CAAAGCCCCTGAATAGGG	6903
		CCCTATTCAAGGGCTTGT	6904
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Cys29Term TGC-TGA	TGGTCTTAGACCACTACCAAGAACATACCCAAAGCCCAGAACATTG GTCTTCTTCCGTTGAGCCACCAATTAAATCTGAGAACAGATTCA CCTTCACCTATACGAAACAGATCGAACATTG	6905
		ACAATTCCGATCTGTTGTAGGTGAAGGTGAAATTCTCTCAGA TTAAATTGGTGGCTAAACGGAAAGAACCCATTCTGGCTTGG GGTATATTCTGGTAGTGGCTAAGACCA	6906
		TCCGTTGAGCCACCAA	6907
		TTGGTGGCTAAACGGGA	6908
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Leu33Term TTA-TGA	CACTACCAAGAACATACCCAAAGCCCAGAACATGGGCTTCCGT TTGCGCCACCAATTGAAATCTGAGAACATTACCTTCACCTATA CGAACAGATCGAACATTGTTGGCATTGAG	6909
		CTCAATGCCAACAAATTCCGATCTGTTGTAGGTGAAGGTGAAA TTCTTCTCAGATTCAATTGGTGGCGAACGGAAAGAACCCATT TCTGGGCTTGGGTATATTCTGGTAGTG	6910
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg36Term AGA-TGA	CACCAATT <u>GAAAT</u> CTGA	6911
		TCAGATT <u>CAATT</u> GGTG	6912
		AGAATATA <u>CCCAAAGCCC</u> AGAATAGGGTCTTCGCGGCCA CCAATTAA <u>ATCTGT</u> GAAGAATT <u>CACCTTCACCTATACG</u> AACAGAT CGGAATTGGTGGGCATTGAGGGTAAGTG	6913
		CACTTACCC <u>CTCAATGCCCAACAATTCCGATCTGTTCGT</u> TAGGTGA AGGTGA <u>AAATTCTTC</u> ACAGAT <u>TTAAATTGGTGGCGAACCGG</u> AAGAA GACCCTATTCTGGGCTTGGGTATATTCT	6914
		TAAATCTG <u>TAAGAATT</u>	6915
		AATTCTTC <u>ACAGATT</u> A	6916
	Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Trp4Term TGG-TGA	CTCTTTATTATCCTCC <u>CTTCTTGT</u> TTTGAG <u>TTCTGAGTCACC</u> TATGGCAAG <u>TTGAGT</u> GATT <u>TCAGAATGTGGGCTAAGGCCACTTCC</u> AAGAAT <u>CTATGCCAGGCC</u> CAGAAG <u>GTGGA</u>	6917
		TCCACTTCTGGGC <u>CTGGC</u> ATAGATT <u>CTTGGAA</u> GTGGC <u>CTTAGCCC</u> ACATT <u>CTGAAATCAC</u> <u>CAACTGCC</u> ATAGGT <u>GACTCAGAACTCAA</u> AAAAACAA <u>AGAGGAGG</u> GATAATAAGAG	6918
		GCAAG <u>TTGAGT</u> GATT <u>TC</u>	6919
		GAAAT <u>CACTCAACTTG</u> C	6920
		TATCCTCCT <u>CTTCTTGT</u> TTTGAG <u>TTCTGAGTCACCTATGGCA</u> AG <u>TTGGGTGATT</u> <u>TGAGAATGTGGGCTAAGGCCACTTCCAAAGAAC</u> TC TATGCC <u>AGGCC</u> CAGAAG <u>GTGGAGCTTCATG</u>	6921
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Ser7Term TCA-TGA	CATGAAG <u>CTCCACTTCTGGGCTGG</u> CATAGATT <u>CTTGGAA</u> GTGGC CTTAG <u>CCCACATTCTCAAA</u> T <u>CCCAACTTGCC</u> ATAGGT <u>GACTCAG</u> AACT <u>CAAAAAAAACAAAGAAGAGGAGG</u> GATA	6922
		GGT <u>GATTGAGAATGTG</u>	6923
		CAC <u>ATTCTCAAA</u> T <u>CACC</u>	6924
		TCC <u>TCCTCTTCTTGT</u> TTTGAG <u>TTCTGAGTCACCTATGGCAAG</u> TTGG <u>GTGATT</u> <u>TCATAAATGTGGGCTAAGGCCACTTCCAAAGAAC</u> AT <u>CTAT</u> GCC <u>AGGCC</u> CAGAAG <u>GTGGAGCTTCATG</u> TT	6925
		AACAT <u>GAAGCTCCACTTCTGGGCTGG</u> CATAGATT <u>CTTGGAA</u> GTG GC <u>CTTAGCCCACATTATGAAATCACCAACTTGCC</u> ATAGGT <u>GACTC</u> AG <u>AACTCAAAAAAAACAAAGAAGAGGAGG</u> GATA	6926
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Glu8Term GAA-TAA	TG <u>ATTTCATAATGTGGG</u>	6927
		CCC <u>ACATTATGAAATCA</u>	6928

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Cys9Term TGT-TGA	CTCTTCTTTGTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGG TGATTCAGAAT <u>GAGGGCTAAGGCCACTCCAAGAATCTATGCCA</u> GGCCCAGAAGTGGAGCTTCATGTTCAAC	6929
		GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGG AGTGGCCTTAGCCC <u>I</u> CATTCTGAAATACCCAACTGCCATAGGTG ACTCAGAACTCAAAAAAAACAAAGAAGAG	6930
		TCAGAACAT <u>GAGGGCTAAG</u>	6931
		CTTAGCCCC <u>I</u> CATTCTGA	6932
		ATGAAGCAGCAACAGTACAAGACACCCCAATTCTAAATGGCGTTA ATGGTTTCTATGCT <u>I</u> AAGAAGAAGAAGAAGAGGATTTCGACTT AAGCAATCCTCCTCCATTCAATATTGGTC	6933
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Lys21Term AAA-TAA	GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTC TTCTTCTTCTTCTT <u>A</u> AGCATGAAAACCATTAACGCCATTAGAATTG GGGTGTCTTGTACTGTTGCTGCTTCAT	6934
		TTCATGCT <u>I</u> AAGAAGAA	6935
		TTCTTCTT <u>A</u> AGCATGAA	6936
		AAGCAGCAACAGTACAAGACACCCCAATTCTAAATGGCGTTAATG GTTTCTATGCT <u>AA</u> ATAAGAAGAAGAAGAAGAGGATTTCGACTTAAG CAATCCTCCTCCATTCAATATTGGTCAGA	6937
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu22Term GAA-TAA	TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC TTCTTCTTCTTCTT <u>ATT</u> AGCATGAAAACCATTAACGCCATTAGAA TTGGGGTGTCTTGTACTGTTGCTGCTT	6938
		ATGCTAA <u>AT</u> AAGAAGAA	6939
		TTCTTCTT <u>ATT</u> AGCAT	6940
		CAGCAACAGTACAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCT <u>AA</u> AGA <u>AT</u> AAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6941
		GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTT <u>ATT</u> CTT <u>TT</u> AGCATGAAAACCATTAACGCCATTAA GAATTGGGGTGTCTTGTACTGTTGCTG	6942
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu23Term GAA-TAA	CTAAAGA <u>AT</u> AAGAAGAA	6943
		TTCTTCTT <u>ATT</u> CTT <u>TT</u> AG	6944
		CAGCAACAGTACAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCT <u>AA</u> AGA <u>AT</u> AAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6945
		GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTT <u>ATT</u> CTT <u>TT</u> AGCATGAAAACCATTAACGCCATTAA GAATTGGGGTGTCTTGTACTGTTGCTG	6946
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu24Term GAA-TAA		
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTAAAGAATAAGAAGAA	6947
	TCTTCTT <u>A</u> TTCTTGTAG	6948
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA AGAACGATCAAGCTTAGTTGATCCAAGTGCTCCACCACCCCTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAA TTTGGAAATTGCTGCTCTGATATTGCAATCTTGAAGGGTGGTGGAA GCACTTGGATCAA <u>A</u> CTAAGCTTGATCTTCTTCCTGCACCATTAC CAACATGTTAGAGGGCTGTGCTTGGACC CAAGCTTAGTTGATCC	6949 6950 6951 6952
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Lys31Term AAG-TAG	GGTAATGGTGCAGGGAAAGAACGATCAAGCTTATTGATCCAAGTG CTCCACCAACCCCTCTAGATTGCAAATATCAGAGCAGCAATTCCAAA ACATTGCTGGAGAAGAACACATTGAGAT ATCTCAATGTGTTCTCTCCCAGCAATGTTGGAAATTGCTGCTCT GATATTGCAATCT <u>A</u> GAAGGGTGGTGGAGCACTTGGATCAAATAA GCTTGATCTCTTCCTGCACCATTACC CACCCCTCTAGATTGCA TGCAATCT <u>A</u> GAAGGGTG	6953 6954 6955 6956
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Arg36Term AGA-TGA	AAAGAACGATCAAGCTTATTGATCCAAGTGCTCCACCACCCCTCA AGATTGCAAATATCT <u>G</u> AGCAGCAATTCCAAAACATTGCTGGAGAA GAACACATTGAGATCTGAGTTATGTT GAACATAACTCAGAGATCTCAATGTGTTCTCTCCCAGCAATGTTT GGAATTGCTGCT <u>C</u> AGATATTGCAATCTTGAAGGGTGGTGGAGCA CTTGGATCAAATAAGCTTGATCTCTT CAAATATCT <u>G</u> AGCAGCA TGCTGCT <u>C</u> AGATATTG	6957 6958 6959 6960
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Leu41Term AAA-TAA	TATTTGATCCAAGTGCTCCACCACCCCTCAAGATTGCAAATATCA GAGCAGCAATTCC <u>A</u> ACATTGCTGGGAGAACACATTGAGATC TCTGAGTTATGTTCTGAGGGATGTGTTGG CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT CTCCCAGCAATGTT <u>A</u> TGGAATTGCTGCTGATATTGCAATCTG AAGGGTGGTGGAGCACTTGGATCAAATA CAATTCC <u>A</u> ACATTGC GCAATGTT <u>A</u> TGGAATTG	6961 6962 6963 6964

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Glu8Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCGCTGACGGCGGGCAATGGC CCGGCTCGTGTCTCC T AGTGCTCGGGCCTCGCCGCCGTCCGCC GCCTGCGCGCCGGCCGGGGCGCCATTGCGGC GCGCCGCAATGGCGCCCCGGCCGGCGCAGGCGGCGGACGG GCGCGAGGCCGAGCACT <u>AGGAGAGCACGAGCCGGG</u> CCATTGC CGCCGTAGCGGGCGGGTGCGGGTGCGGGTGGATG	6965
		TGCTCTCC T AGTGCTCG	6967
		CGAGCACT <u>AGGAGAGCA</u>	6968
		ACCCGCACCCGCACCCGCCCGCTGACGGCGGGCAATGGCCC CTCGTGTCTCCGAGTG <u>A</u> TCGGGCCTCGCGCCCGTCCGCC GCGCGCCGGCCGGGGCGCCATTGCGGCCGGTCA	6969
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Cys9Term TGC-TGA	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCAGGCGGCGG ACGGGCGCGAGGCC <u>G</u> ATCACTCGGAGAGCACGAGCCGGG TTGCCGCCGTAGCGGGCGGGTGCGGGTGCGGGTGCGGGT	6970
		TCCGAGTG <u>A</u> TCGGGCCT	6971
		AGGCCCG <u>A</u> TCACTCGGA	6972
		CCGCACCCGCACCCGCCCGCTGACGGCGGGCAATGGCCC CGTGCTCTCCGAGTG <u>C</u> AGGGCCTCGCGCCCGTCCGCC GCGCGGGCCGGGGCGCCATTGCGGCCGGTCA GGTGACCCGCCGCAATGGCGCCCCGGCCGGCGCAGGGGG GGACGGGCGCGAGGCC <u>T</u> AGCACTCGGAGAGCACGAGCCGG CATTGCCGCCGTAGCGGGCGGGTGCGGGTGCGGGTGC CGAGTG <u>C</u> AGGGCCTCG	6973
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser10Term TCG-TAG	6974	
		6975	
		CGAGGCC <u>C</u> TAGCACTCG	6976
		GCTCGGGCTCGCGCCCGTCCGCCGCCTGCGCGCCGGGGGG CGCCATTGCGCGCGGTGACCCCCCGCGCTCTCCGCC CGCGTGTCCCGCGTCCCGTCCATCCACCGCGA TCGCGGTGGATGGACCGGGACCGGGACCGGGCGGGCGCC CGGAGAGCGCGGGGGGT <u>C</u> ACCGCGCCGCAATGGCGCCCC GGCGCGCAGGCCGGACGGCGCGAGGCCGAGC GGCGCGGT <u>G</u> ACCCCCCG	6977
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser29Term TCA-TGA	6978	
		6979	
		CGGGGGGT <u>C</u> ACCGCGCC	6980
		CCCCCTCCCCACGCACACGCACAGATCCATCCGCC CCCCGCAATGAGGCC <u>G</u> TAGCAGGAGGCCAGCTGCAAGGCCACC GAGGACCAACCGCTCGAGTTGACGCCCAAGC	6981
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu8Term GAG-TAG	GCTTGGCGGCGTGA <u>ACT</u> CGGAGCGGGTGGTCTCGGTGGCCTTG CAGCTGCCCTCTGCT <u>A</u> CGGCCCTATTGCGGGGGCATGCCGC	6982
		GGATGGATCTGTGCGTGTGCGTGGGGAGGGGG	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Gln9Term CAG-TAG	TGAGGCCGTAGCAGGAG	6983
	CTCCTGCTACGGCCTCA	6984
	CCTCCCCCACGCACACGCACAGATCCATCCGCCATGGCCCC CGCAATGAGGCCGGAGTAGGAGGCAGCTGCAAGGCCACCGAG GACCACCGCTCCGAGTCGACGCCCAAGCCGC	6985
	GCGGCTTGGCGCGTCGAACTCGGAGCGGTGGTCTCGGTGGC CTTGCAGCTCGCCTCTACTCCGGCCTCATTGCGGGGGCCATGG CCGGGATGGATCTGCGTGTGCGTGGGGAGG	6986
	GGCCGGAGTAGGAGGCG	6987
	CGCCTCCTACTCCGGCC	6988
	CCCCCACGCACACGCACAGATCCATCCGCCATGGCCCCCGC AATGAGGCCGGAGCAGTAGGCGAGCTGCAAGGCCACCGAGGACC ACCGCTCCGAGTCGACGCCCAAGCCGC	6989
	GCGGCGGCTTGGCGCGTCGAACTCGGAGCGGTGGTCTCGGT GGCCTTGCAGCTCGCCTACTGCTCCGGCCTCATTGCGGGGGCCA TGGCCGGATGGATCTGCGTGTGCGTGGGG	6990
	CGGAGCAGTAGGCGAGC	6991
	GCTCGCCTACTGCTCCG	6992
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu10Term GAG-TAG	ACGCACAGATCCATCCGCCATGGCCCCCGCAATGAGGCCGG AGCAGGAGGCAGCTGAAAGGCCACCGAGGACCACCGCTCCGA GTTGACGCCGCCAGCCGCCCTCCGCATC	6993
	GATGCGGAAGGGCGCGCTGGCGCGTCGAACTCGGAGCGG TGGTCCTCGGTGGCCTTCAAGCTCGCCTCTGCTCCGGCCTCATT GCGGGGGCCATGGCCGCGGATGGATCTGCGT	6994
	GCGAGCTGAAAGGCCAC	6995
	GTGGCCTTCAAGCTCGC	6996
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Cys13Term TGC-TGA	CTTCACAAATCACAAATCGGAATCAGATCCACCAAGACACCCGG CGGCAATGGCGCGTAGGGCACCCAGGGAGGCCACTGCAAGGC TTCCGAGGACGCCCTCTCTTCGACGCC	6997
	GCGGCGTCGAAGAAGAGACGGCGTCCTCGGAAGCCTGAGTC GGCCTCCTGGTGCCTACGCCGCCATTGCCGCCGGGTGCGT GGTGGATCTGATTCCGATTGTGATTGTGAAG GGCGCGTAGGCACCC	6998 6999
		7000

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCA CGACACCCCCGGCGGCAATG GCGGCCTCGGCGACCTAGGAGGCCACTGCAAGGCTTCCGAGG ACGCCCGTCTCTTCGACGCCGCCAAGCCCC	7001
		GGGGCTTGGCGGGCTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAGTCGGCCTCCTAGGTGCGCGACGCCGCCATTGCCGCCG	7002
		GGGTGTCTGGTGGATCTGATTCCGATTGTGAT	7003
		CGGCGACCTAGGAGGCC	7004
		GGCCTCTTAGGTGCCG	7004
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCA CGACACCCCCGGCGGCAATGGC GGCGTCGGCGACCCAGTAGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCGACGCCGCCAAGCCCCGC	7005
		GCGGGGGCTTGGCGGCCTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGAGTCGGCCTACTGGTCGCCGACGCCGCCATTGCCG	7006
		CCGGGGTGTCTGGATCTGATTCCGATTGT	7007
		CGACCCAGTAGGCCGAC	7008
		GTCGGCCTACTGGTCG	7008
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Cys10Term TGC-TGA	TCAGATCCACCA CGACACCCCCGGCGGCAATGGCGCGTCGGCGA CCCAGGAGGCCGACTGAAAGGCTTCCGAGGACGCCGTCTCTC TTGACGCCGCCAAGCCCCGCCCTCCGCATC	7009
		GATGCGGAAGGGGGGGCTTGGCGGCCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTTICAGTCGGCCTCTGGTCGCCGACGC CGCCATTGCCGCCGGGTGTCGTGGATCTGA	7010
		GCCGACTGAAAGGCTTC	7011
		GAAGCCTTICAGTCGGC	7012

WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications of the oligonucleotide, said chemical modifications selected from the group consisting of an o-methyl modification, an LNA modification including LNA derivatives and analogs, two or more phosphorothioate linkages on a terminus, and a combination of any two or more of these modifications.
2. The oligonucleotide according to claim one that comprises two or more phosphorothioate linkages on at least the 3' terminus.
3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.
4. The oligonucleotide according to claim one that comprises an LNA nucleotide, including an LNA derivative or analog.
5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.
6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.
7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 4341-7012 .
8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in callus, comprising administering to the callus an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A plant organism comprising the cell according to claim 14.

16. A plant or plant part produced by the method of claim 11.

17. A method of determining whether an oligonucleotide is optimized for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a second oligonucleotide, said second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2'-O-methylated oligonucleotide and a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

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18. The method of claim 17 in which the alteration is produced in a plant cell extract.
19. The method of claim 17 in which the alteration is produced in a cell.
20. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2-O-methylated oligonucleotide and a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

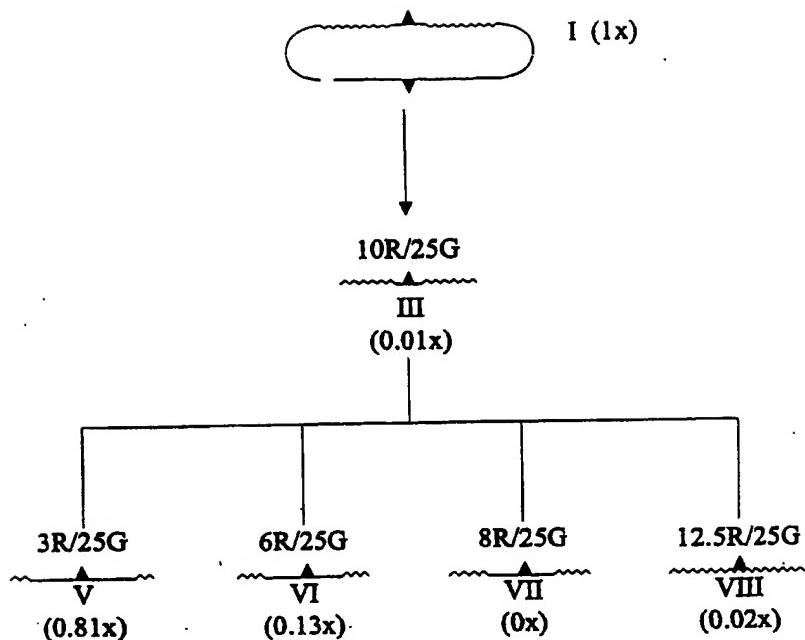


Figure 1A

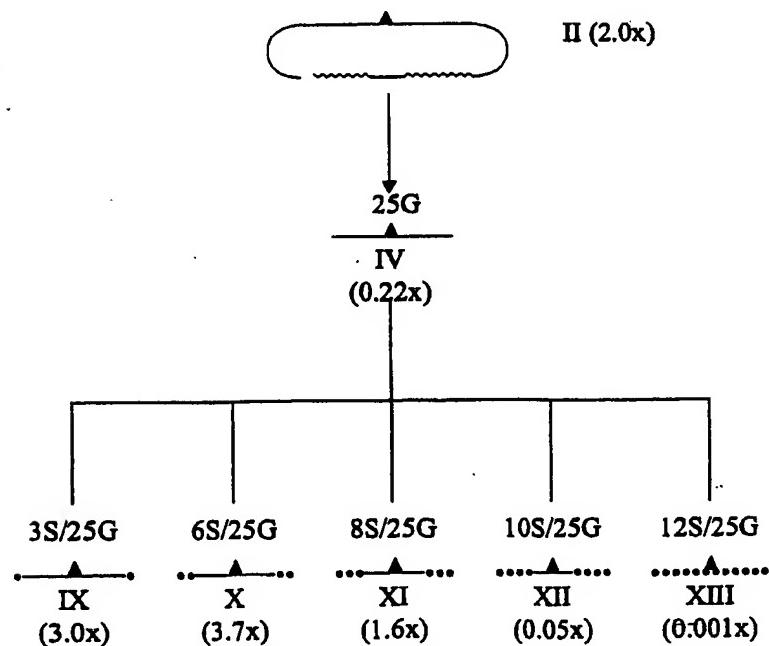


Figure 1B

SUBSTITUTE SHEET (RULE 26)

Plasmids, DNA targets and chimeric oligonucleotides

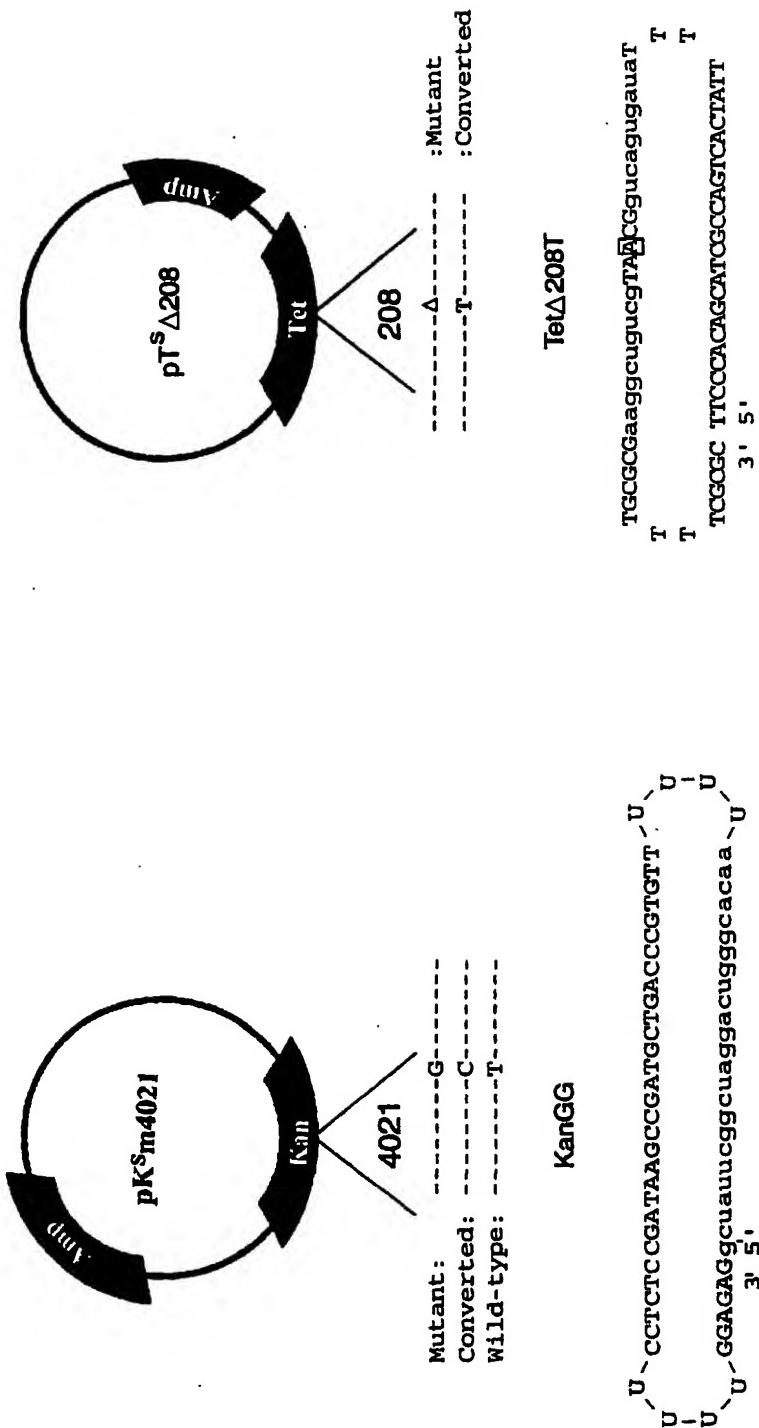


Figure 1C

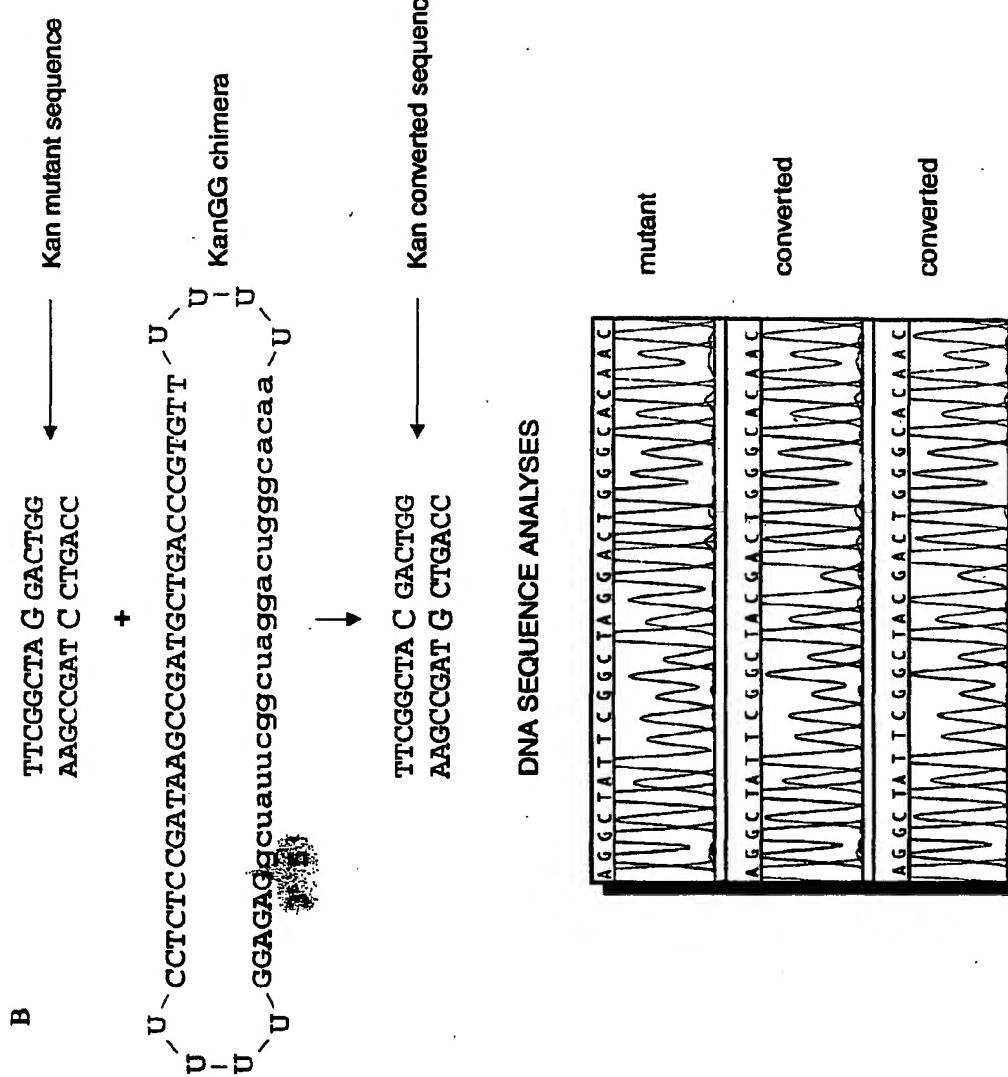


Figure 1D

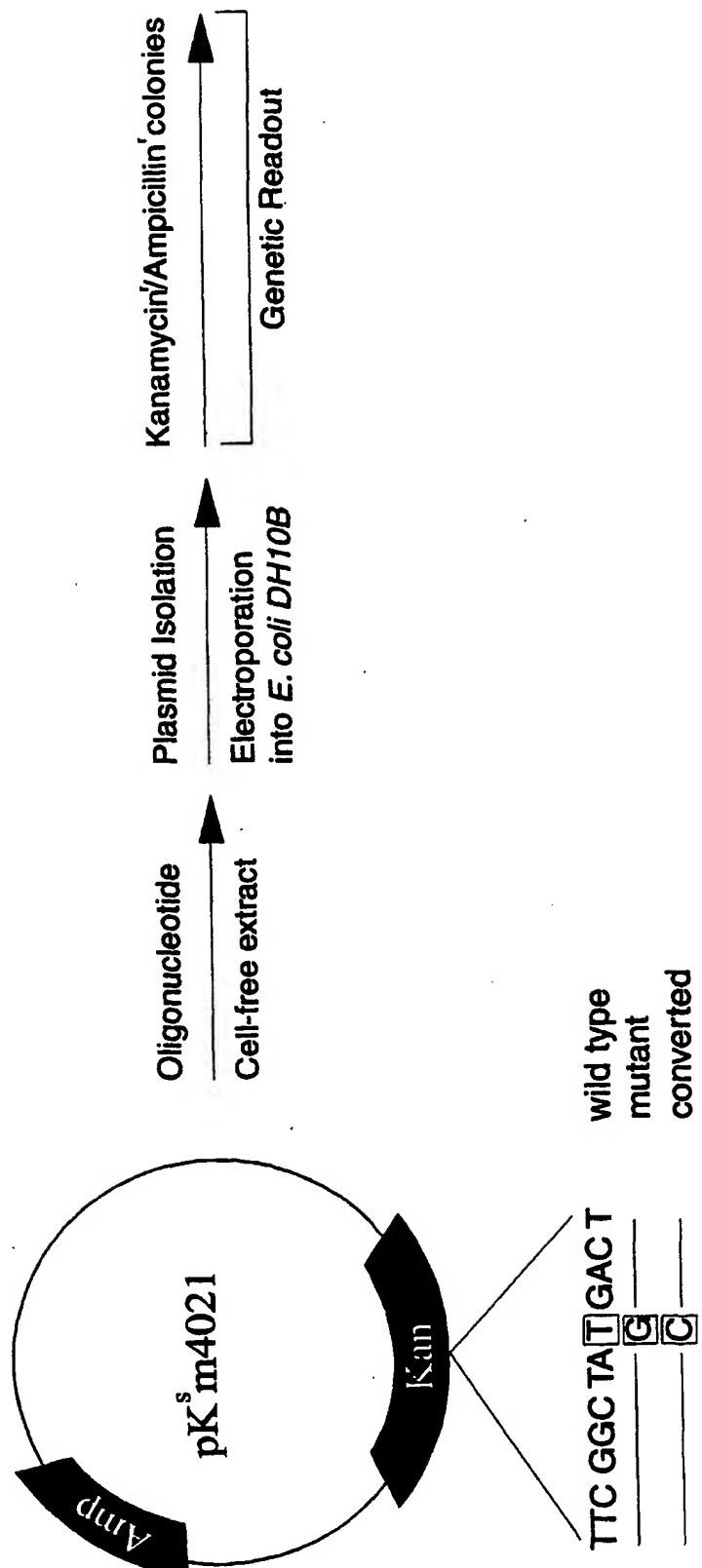
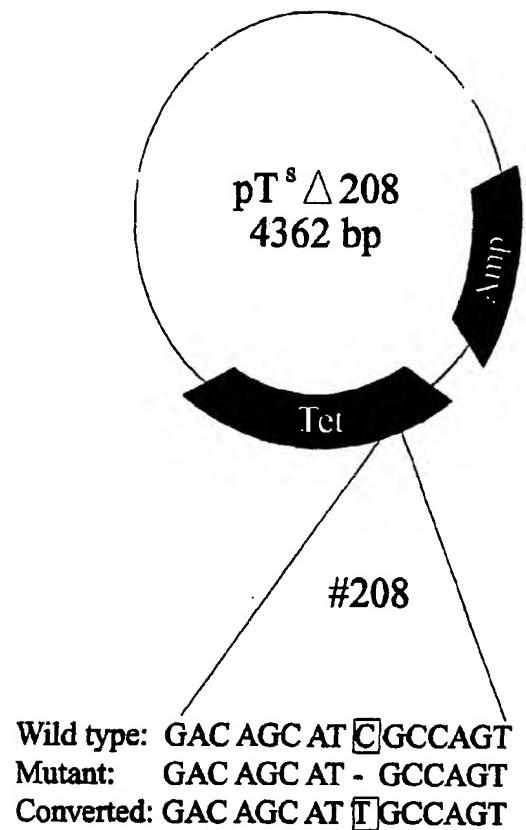


Figure 2



Sequence analysis of Tet^r plasmid Δ208

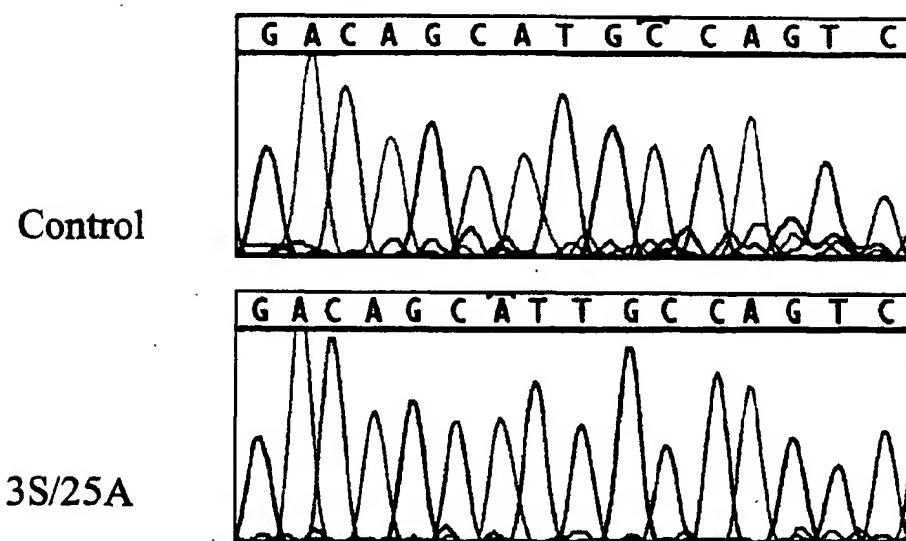


Figure 3

DNA sequence analysis of Kan^r plasmids

Target codon distribution					
oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	---	+	—	—	—
2) 6S/25G (20)	—	+	—	—	—
3) 8S/25G (20)	—	+	—	—	—
4) 10S/25G (18)	—	+	—	+(2)	+(2)
5) 25S/25G (4)	—	—	+(2)	+(2)	—

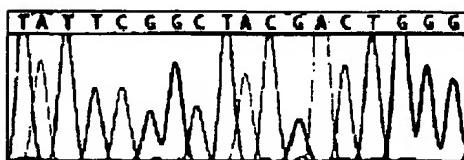
3S/25G



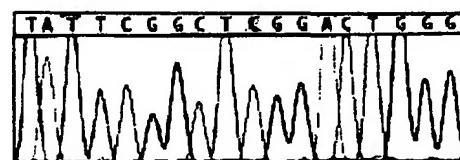
6S/25G



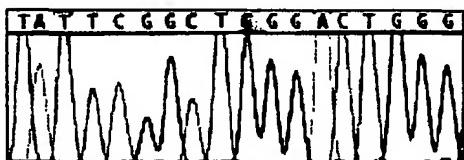
8S/25G



10S/25G



25S/25G



25S/25G

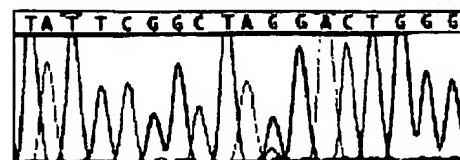


Figure 4

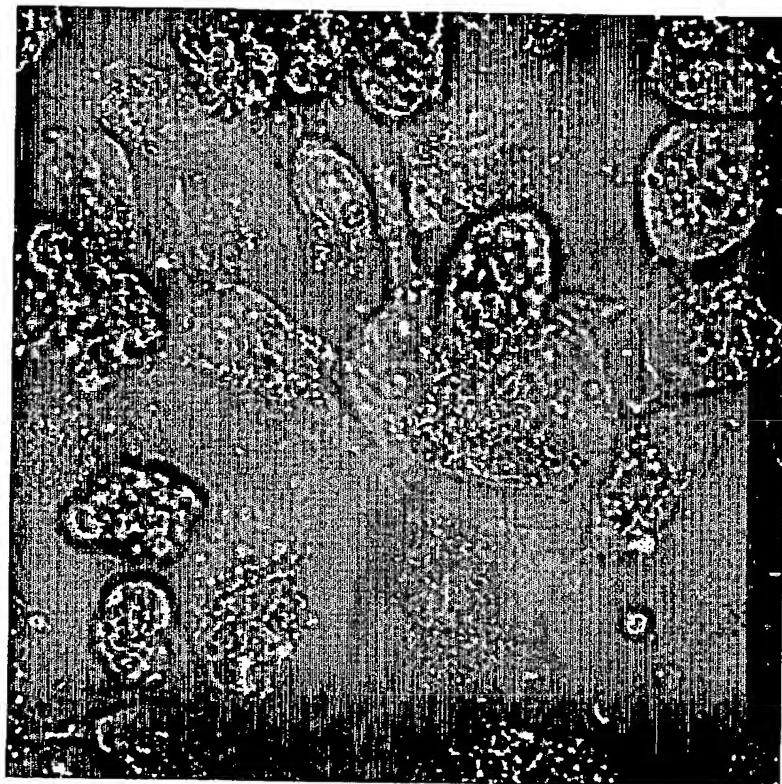


Figure 5

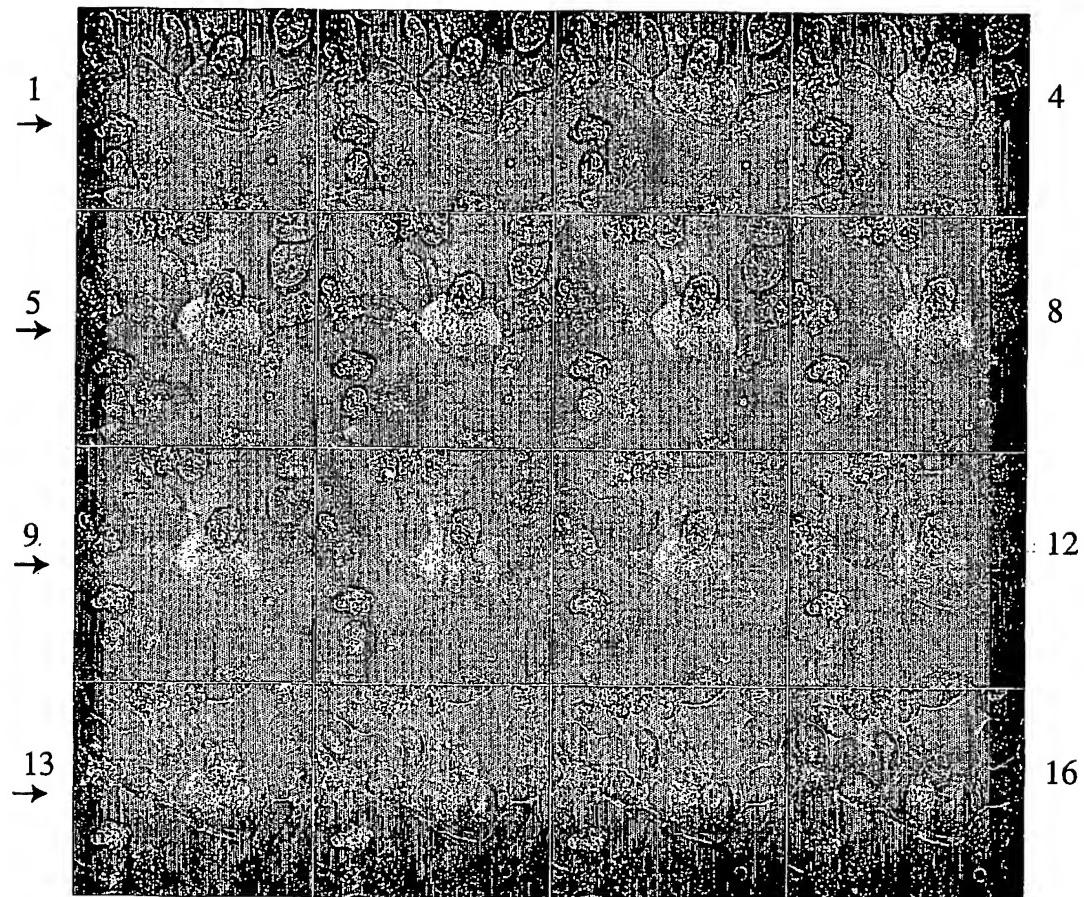
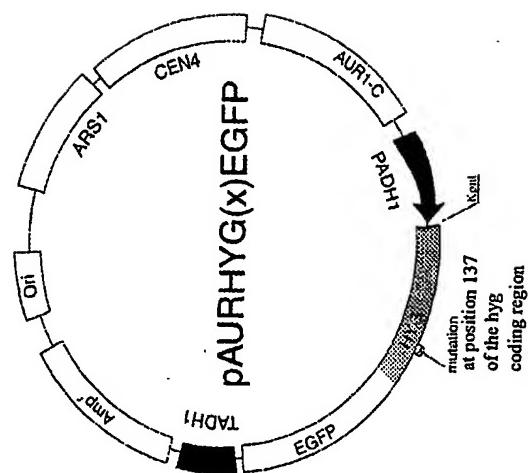


Figure 6

Sequence of normal allele: GTGGATAATGTCCCT
 Target/existing mutant: GTGGATAAATGTCCCT
 Desired alteration:

Figure 7A



Sequence of normal allele: GTGGATAATGTCCCT
 Target/existing mutant: GTGGATAGGTCCCT
 Desired alteration:

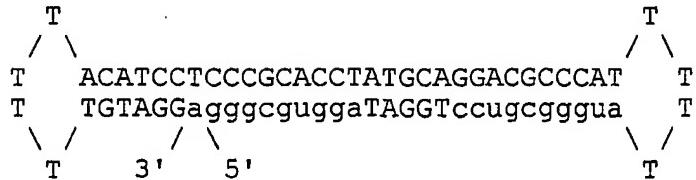
Figure 7B

HyqE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HyqE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC
GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG
CCG ATG GTT TCT AC-3'

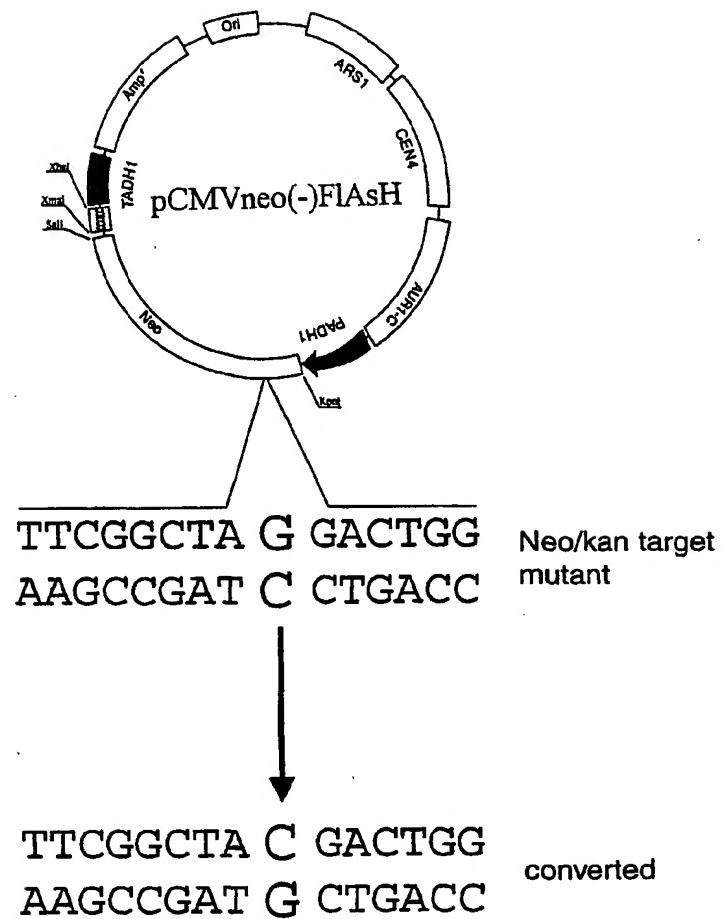
HyqE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG
CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA
GCT GAA AGC ACG AG-3'

HyqGG/Rev:



Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT
CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG
A-3'

Figure 8



FUSION GENE FOR LIGAND BINDING

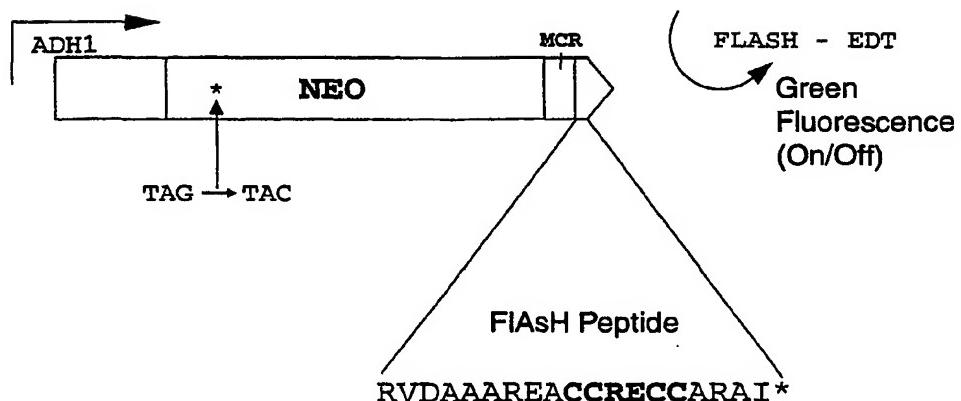


Figure 9

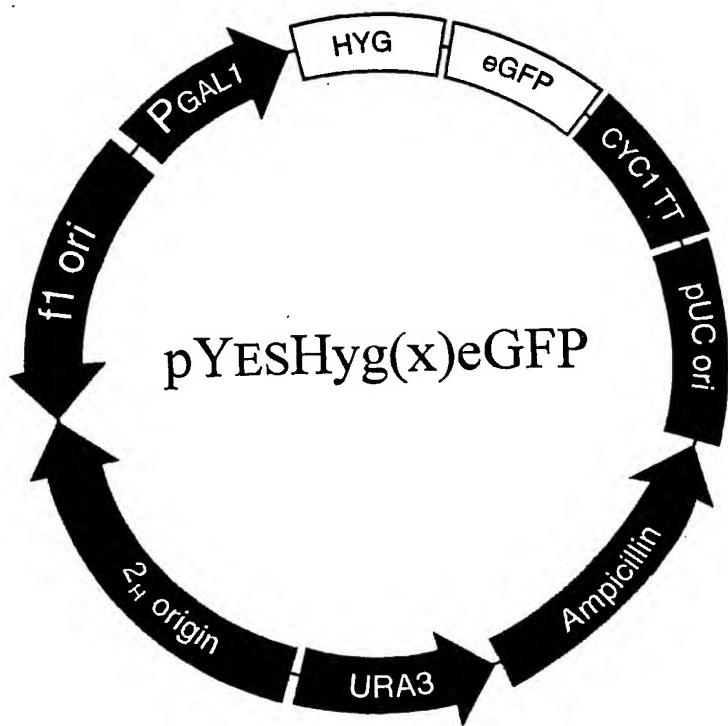


Figure 10

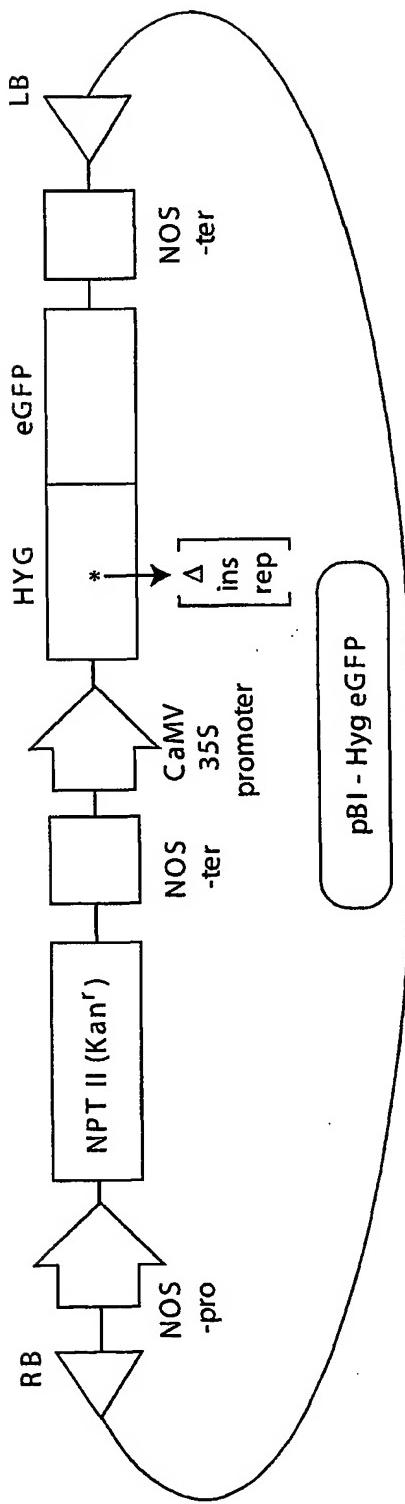


Figure 11